Run on:

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TELBEAX: (312)
TELBEAX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: AMINO ACID
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                                                                     June 26, 2005, 12:10:37; Search time 30.1562 Seconds (without alignments) 2279.856 Million cell updates/sec
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-479-532-39
US-08-455-526-39
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US-09-139-491-39
US-09-134-250-5
US-09-883-825-39
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US-08-455-526-45
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US-09-139-491-45
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US-09-139-491-43
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Patent No. 5389527

GENERAL INFORMATION:

APPLICANT: Bearov. Joseph A.

APPLICANT: Bentley, Kelley

APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.

TITLE OF INVENTION: Phosphodiesterases

NUMBER OF SEQUENCES: 58

CORRESPONDENCES: 58

CORRESPONDENCES: 58

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: Street

STREET: Street

STREET: Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: BACentlin Release #1.0, Version #1.25
SOUTHWER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5389527and, Greta E.
REGISTRATION NUMBER: 35,302
***COMPUTED NUMBER: 35,302
***COMPUTER: NUMBER: 27866/30822
US-09-883-825-45
US-09-708-392-5
US-09-949-016-6244
PCT-US92-0322-45
US-09-754-250-4
US-09-754-250-4
US-08-951-648-6
US-09-174-437-6
US-09-174-437-4
US-09-174-437-4
US-09-174-437-4
US-09-174-437-4
US-09-174-437-4
US-09-174-437-2
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US-08-880-55A-2
US-08-880-55A-2
US-08-880-55A-2
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TELECOMMUNICATION INFORMATION:
                           941
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STATE: Illinois
COUNTRY: USA
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US-07-872-644-39
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                                                                                              YTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAP
                                                                                                                                                  DTQVLV1PLVDKEAGAVAAV1LVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSV
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     Best Local Similarity 100.
Matches 921; Conservative
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Sequence 39, Application US/08297494 Patent No. 5580771 GENERAL INFORMATION:

RESULT 2 US-08-297-494-39

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                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, STREET: Two First National Plaza, 20 South Clark STREET: Street
STREET: Carpe First Carpe CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATE: PSTERM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mamma.
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMOUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5580771and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 921; Conservative
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                                                                                                                                                                                                                                                                                                               ZIP: 60603
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100.0%; Pred. No. 0;
tive 0; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 394-5750
TELEFAX: (312) 394-5740
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       LENGTH: 921 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 921; Conservative
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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ZIP: 60603

CMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
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Patent No. 5602019
GENERAL INFORMATION: Geoph A. APPLICANT: Beavo, Joseph A. APPLICANT: Carbonneau, Harry APPLICANT: Carbonneau, Harry APPLICANT: Sonnenburg, William K. TITLE OF INVENTION: Phosphodiesterases NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
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     61 YTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAP 120
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APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Connenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalia
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
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; GENERAL INFORMATION:
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SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
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CITY: CLICAGO
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
PILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/297,494
FILING DATE: 07-JUN-1995
RILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5776752BAIG, GRECHE E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
REFERENCE/DOCKET NUMBER: 27866/30822
REFERENCE/DOCKET NUMBER: 27866/30822
REFERENCE/DOCKET NUMBER: 27866/30822
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Bearo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
TITLE OF INVENTION: Phosphodiesterases
CORRESPONDENCE ADDRESS:
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                                                                                                                              EVPDLDGARAPINGCCSLDAE 921
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TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 921, Conservative
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                                                 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
                                                                                                           QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
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                   NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
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GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: Phosphodiesterases
ITILE OF SEQUENCES: 58
CORRESPONDERSS: ADDRESS:
ADDRESSE: Marchall, O'Toole, Gerstein, Murray & ADDRESSE: Bicknell;
STREET: The First National Plaza, 20 South Clark
STREET: Street
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COMPUTER READABLE FORM:
MEDIUM TRYEE Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
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APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
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; Patent No. 5800987
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STATE: Illinois
COUNTRY: USA
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US-08-455-525-39
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ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
ZIP: 60603
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,526
FILING DATE: 31-MAY-1995
CLASSIFICATION NUMBER: US 08/297,494
FILING DATE: 04-APR-1991
ATPONENT/AGENT INFORMATION:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATPONENT/AGENT INFORMATION:
APPLICATION NUMBER: 35,302
ATPONENT/AGENT INFORMATION:
TELEPHONE: (312) 984-9740
TELEPHONE: (312) 984-9740
TELEPAX: (312) 984-9740
TELEPAX: SCA-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TELENTA: 1921 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603

ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,491
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100.0%; Pred. No. 0;
tive 0; Mismatches
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APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6015677and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEFRON: (312) 946-5750
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
ITILE OF INVENTION: Dhosphodiesterases
TITLE OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
                                                 901 EVPDLDGARAPINGCCSLDAE 921
                                                                                      901 EVPDLDGARAPINGCCSLDAE 921
                                                                                                                                                                                      ; Sequence 39, Application US/09139491
; Patent No. 6015677
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INFORMATION FOR SEQ ID NO: 39:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Best Local Similarity
Matches 921; Conserv
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CLASSIFICATION:
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100.0%; Pred. No. 0;
| TELEPHONE: (312) 346-5750
| TELEFAX: (312) 984-9740
| TELEX: 25-3856
| INFORMATION FOR SEQ ID NO: 39:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 921 amino acids
| TYPE: amino acids
                                                                                                                                                                                                                                                                Matches 921; Conservative
                                                                                                                                                             / MOLECULE TYPE: protein
US-08-455-525-39
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Best Local Similarity
                                                                                                                                           TOPOLOGY:
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                                           DB 3;
                                        Query Match 100.0%; Score 4781; Best Local Similarity 100.0%; Pred. No. 0; Matches 921; Conservative 0; Mismatches
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Sequence 5, Application US/09754250

Patent No. 637622

GENERAL INFORMATION:

APPLICANT: WELL MAING-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/754,250

CURRENT APPLICATION DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 921

TYPE: PRT
                                                                                       241 CCLLLVSEDNLQLSCKVIGDKVLEREISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQ.
241 CCLLLVSEDNLQLSCKVIGDKVLEREISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQ.
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; Sequence 39, Application PC/TUS9203222
; GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: Phosphodiesterases
ITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/0813,825
FILING DATE: UNKNOWN-
PRIOR APPLICATION NUMBER: 09/123,783
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: 08/297,494
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: US 07/688,356
FILING DATE: CONKNOWN-
APPLICATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELECOMMUNICATION INPORMATION:
TELERAN: (312) 346-5750
TELERAN: (312) 346-5750
TELEBRAX: (312) 346-5750
                                                                                                                                                                                                                                                                      STREET: Two First National Plaza, 20 South Clark
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                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
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                                                                      APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnehburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-883-825-39
US-09-883-825-39
; Sequence 39, Application US/09883825
; Patent No. 6642040
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 921 amino acids
                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      Bicknell
                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Simil
Matches 921, C
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HGCNI FDHFSRKDYQRMLDLMRDI ILATDLAHHLRI FKDLQKMAEVGYDRTNKQHHSLLL
                                                                                                    HGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKDLQKMAEVGYDRTNKQHHSLLL
                                                                                                                                                              CLLMTSCDLSDQTKGWKTTRKIABLIYKBPFSQGDLBKAMGNRPMEMMDREKAYIPELQI
                                                                                                                                                                                  CLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION NUMBER: US/07/88,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 346-5760
TELEFAX: (312) 384-9740
TELEFAX: (312) 384-9740
TELEFAX: MAINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
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CORRESPONDENCE ADDRESS:
ADDRESSER: Marchall, O'Toole, Geretein, Murray &
ADDRESSER: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
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; Pred. No. 0;
3; Mismatches
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Patent No. 5389527
GENERAL INFORMATION:
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Best Local Similarity 98.9
Matches 898; Conservative
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STATE: Illinois
COUNTRY: USA
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US-07-872-644-43
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US92/0322
FILNG DATE: 19920420
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATPONEY/AGENT INPORMATION:
NAMB: NO.land, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPRAX: (312) 946-9740
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: AMINO ACID
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 921; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL 853
73
                      94
              35 EPPPPPQPCADSLQDALLSLGSVIDVAGLQQAVKBALSAVLPKVETVYTYLLDGESRLVC
                                                  EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE
                                                                  EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE
                                                                                                                       AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                                                                                                          GDQKGGVAYTDQDKKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
                                                                                                                                                                                                                               SCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV
                                                                                                                                                                                                                                                                                    PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC
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                                                                                                                                                                                                                                                                                                                                                                                              SYEIRIPADQEIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQE
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QEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTYLLDGESRLVC
                                                                                                        AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                                                                                            GDOKGGVAYTNODRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
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Sequence 43, Application US/08297494
Patent No. 5580771
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry

RESULT 12 US-08-297-494-43

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APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STRTE: Illinois
COUNTRY: USA
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILLING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 55807/1and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEBRAX: (312) 984-9740
TELEBRAX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEGUINCE CHARACTERISTICS:
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98.9%; Pred. No. 0;
ative 3; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
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amino acid
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Best Local Similarity 98.9
Matches 898; Conservative
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                                                                                                                                                                                                                                                                                                                    97.4%; Score 4657; D
98.9%; Pred. No. 0;
iive 3; Mismatches
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEFRAM: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  LENGTH: 942 amino acida
TYPE: amino acid
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Matches 898; Conservative
                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
    APPLICANT: Beardow, Joseph A.
    APPLICANT: Charbonneau, Harry
    APPLICANT: Charbonneau, Harry
    APPLICANT: Sonnenburg, William K.
    TITLE OF INVENTION: Phosphodiesterases
    NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
    STREET: Two Pirst National Plaza, 20 South Clark
    STREET: Two Pirst National Plaza, 20 South Clark
    STREET: Usa
    COUNTRY: USA
    Illinois
    COUNTRY: USA
    ILL GOO3
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOPENTER: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/297,510
    PRIOR APPLICATION NATA:
    CLASSIFICATION NATA:
    CLASSIFICATIO
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APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
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Sequence 43, Application US/0845526

Patent No. 5789525

GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bearley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Connenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATON PC-DOS/MS-DOS
SOFTWARE: DATON DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-UNN-1995
PILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. S77672AAD (Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                  Sequence 43. Application US/08479532
Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Beavio, Joseph A.
APPLICANT: Beniey, Kelley, APPLICANT: Beniey, Kelley, APPLICANT: Sonnenburg, William K.
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Geretein, Murray & ADDRESSEE: Bicknell.
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98.9%; Pred. No. 0;
iive 3; Mismatches 7;
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TELEFAX: (312) 984-9740
TELEX: 52-3856
INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 942 amino acids
TYPE: amino acid
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898; Conservative
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CITY: Chicago
STATE: 111inoie
COUNTRY: USA
ZIP: 60603
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COMPUTER INEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,526
FILING DATE: 31-MAY-1995
CLASSIFICATION NUMBER: US 08/297,494
FILING DATE: 29-AG-1994
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 35,302
RESTERRENCE/DOCKET NUMBER: 35,302
RESTERRENCE/DOCKET NUMBER: 35,302
FILERAX: 1312) 346-5750
TELEFONMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION SEG 10 NO: 43:
ELOTH: 942 amino acide
TYPE: mino acide
TYPE: procein
US-08-455-526-43
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Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7;
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                                                                                                                                                                         MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD
                                                                                                                                                MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD
                                                                                                                                                                                                                                                          KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL
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                                                          IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC
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Sequence 15, Appl Sequence 2, Appli Sequence 39, Appli Sequence 14, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli

Sequence 15, Sequence 6, A Sequence 2, A

Sequence

Sequence 13, 1 Sequence 3, 1 Sequence 3, 1 Sequence 23, Sequence 5, 1 Sequence 1,

Sequence 2928, Ap Sequence 2944, Ap Sequence 30, Appl Sequence 30, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appli Sequence 5, Appli

Sequence 4

Perfect score:

.. 0

Run

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COURSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: 08/297,494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark
                                   US-10-094-928-1
US-10-104-094-928
US-10-104-047-2928
US-10-104-047-2928
US-10-104-049-30
US-10-86-949-30
US-09-891-216-12
US-09-891-216-14
US-10-86-940-20
4 US-10-26-144-5
4 US-10-26-144-5
4 US-10-26-144-5
14 US-10-168-402-3
15 US-10-168-402-3
15 US-10-440-998-2
15 US-10-440-998-2
15 US-10-440-998-2
15 US-10-440-998-2
15 US-10-440-998-2
15 US-10-440-998-2
15 US-10-618-252-2
15 US-10-618-252-1
15 US-10-618-252-1
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15 US-10-618-252-1
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17 US-10-618-252-1
17 US-10-10-801-1
17 US-10-10-801-2
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TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
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US-10-427-222-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-883-825-39
; Sequence 39, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Bentley, Realley
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Charbonneau, Harry
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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845.5
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     Sequence 39, Appl
Sequence 39, Appl
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Sequence 2, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
                                                                                                                                                                                            June 26, 2005, 12:21:57; Search time 114.692 Seconds (without alignments) 3087.987 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                            4781
1 MRRQPAASRDLFAQEPVPPG......VPDLDGARAFINGCCSLDAE 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_MEW_PUB_pep:*
4: /cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB_pep:*
5: /cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB_pep:*
6: /cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB_pep:*
7: /cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB_pep:*
8: /cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB_pep:*
9: /cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB_pep:*
9: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
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13: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
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18: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
19: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
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10: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
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19: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-094-989-5

US-10-697-894-39

US-09-883-825-43

US-10-697-894-43

US-10-697-894-43

US-10-094-989-2

US-09-883-825-45

US-09-883-825-45

US-10-686-390-5

US-10-686-380-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1717557 seqs, 384547976 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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1000.0
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94.0
993.6
993.6
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4474.5

5 6 10 11

Score

Result Š.

840 900 900

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Sequence 5, Application US/10084989;
Publication No. US20020115179A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PROSPEDIES PROTEINS, MUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001063DIV;
CURRENT PELLING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NOS: 5
    SFMEHIAMPIYKLLODLFPKAABLYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAP
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                                                                                                                  SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTYLLDGESRLVCEBPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAP
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                                                     CLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRRQPAASRDLFAQEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAFOKEOKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                              EVPDLDGARAPINGCCSLDAE
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Matches 921; Conservative
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US-10-094-989-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OYRSHLANEMMYYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
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                                                                                                                                                                                                                                                                                                                                                                                                     APEATQNPPEEAAGDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL
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                                                                                                                                                                                                                                                                                                                       Length 921;
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FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
REPERRENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
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100.0%; Pred. No. 0;
tive 0; Mismatches
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-883-825-39
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 921; Conservative
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ER: 27866/30822
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Pred. No. 0;
; Mismatches
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPAX: (312) 346-5750
TELEFAX: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                  Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 921; Conservative 0;
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Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/10697894
Publication No. US20040126866A1
GENERAL INFORMATION:
APPLICANT: Bentley, Kelley
Charbonneau, Harry
Sonneburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
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APPLICATION NUMBER: US/09/123,783
FILING DATE: 28-U11y-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIR Release #1.0,
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APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-OCt-2003
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCES: 58
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STATE: Illinois
COUNTRY: USA
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                  EEPPHELPOEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE
                                                                               155 AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                                                                                215 GDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
                                                                                                                                                                                                            SCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV
                                                                                                                                                                                                                                                          PVISRATDQVVALACAFNXLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC
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                                                                                                                                                                                                                                                                                                                                                                                     SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK
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                                                             AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                                                            GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
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US-10-697-894-43
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                               SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
                                                SFWEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
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                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                    Bicknell
STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/883,825

FILING DATE: 18-Unn-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/123,783

FILING DATE: «Unknown»

APPLICATION NUMBER: 09/297,494

FILING DATE: «Unknown»

APPLICATION NUMBER: 08/297,494

FILING DATE: «Unknown»

APPLICATION NUMBER: US 07/688,356

FILING DATE: 04-APR-1991

ATORNEY/AGENT INFORMATION:

NAME: No. US20020151024Aland, Greta B.

REFERENCE/DOCKET NUMBER: 35,302

REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                       Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σij.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-883-825-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                              EVPDLDGARAPINGCCSLDAE 921
                                                                                                                  EVPDLDGARAPINGCCSLDAE 921
                                                                                                                                                                                                       Sequence 43, Application US/09893825
Patent No. US20020151024A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 942 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                         APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
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Matches 898; Conservative
                                                                                                                                                                                                                                                                                                                                                       SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                     Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF
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US-09-883-825-43
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILLS REFERENCE: 21402-42C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT PILING DATE: 2003-01-06
PRIOR PAPLICATION NUMBER: US60/318,120
PRIOR PLING DATE: 2001-09-01
PRIOR PILING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-17
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2001-09-17
PRIOR PLING DATE: 2001-09-19
                                                    455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFFPIKNENQE
                                                                                                                                                       635 IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMBIFALFISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 78, Application US/10236417; Publication No. US20040048256A1; GENERAL INFORMATION:
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                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-OCL-2003
FILING DATE: 30-OCL-2003
PRIOR APPLICATION NUMBER: US/99/123,783
FILING DATE: 28-July-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: 28-July-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: 4Uknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: 4Uknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: 04-APR-1991
ATTONBY/AGENT INFORMATION:
NAME: Noland, Greta B.
REGISTRATION NUMBER: 35,302
RELERBANCE/DOCKET NUMBER: 35,302
TELEBRANCE/DOCKET NUMBER: 35,302
TELEBRANCE (312) 346-5750
TELEBRANCE (312) 984-9740
TELEBRANCE (312) 984-9740
TELEBRANCE CHARACTERISTICS:
LENGTH: 942 mmino acids
LENGTH: 942 mmino acids
                                                                        STREET: Two First National Plaza, 20 South Clark
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | LENGTH: 942 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-10-697-894-43
                                                    Bicknell
                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                 94.9%; Score 4539.5;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-78
                                Query Match
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US-10-094-989-2

Sequence 2, Application US/10084989

Publication No. US20020115179A1

Publication No. US20020115179A1

Publication No. US20020115179A1

Publication No. US20020115179A1

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PHOSPHODIESTERASE ENCODING HUMAN

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/094,989

CURRENT PILING DATE: 2002-03-12

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 5

NUMBER OF SEQ ID NOS: 5

LENGTH: 920

LENGTH: 920
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94.8%; Score 4533.5;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 872; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapien
US-10-094-989-2
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                                                                                                                          GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
                                              QEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTYLLDGESRLVC
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ed. No. 0;
Mismatches
 Pred. No.
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US-10-697-894-45
; Sequence 45, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:
              21;
 94.78;
                 Conservative
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Local Similarity
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                            HGCNI FDHFSRKDYQRMLDLMRDI I LATDLAHHLRI FKDLQKMAEVGYDRTNKQHHSLLL
                                                                         CLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION OF CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                     Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: No. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27866/30822 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: *CUNKNOWN>
APPLICATION NUMBER: 08/297,494
FILING DATE: *CUNKNOWN>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%; Score 4474.5;
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                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/0983325
Patent No. US20020151024A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID
US-09-883-825-45
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INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-09-883-825-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER
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Sequence 5, Application US/10686390
Publication No. US20040254153A1
GENERAL INFORMATION:
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US-10-686-390-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAVAAVILVHCGOLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATONPPEEAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL 253
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                                                                                                                                                                                                                                                      COMPUTER: IDDPy disk
COMPUTER: IBM PC Compatible
COMPUTER: PAGE COMPATIBLE
COMPUTER: PAGE COMPATIBLE
COMPATES: PAGE COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-Oct-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/123,783
FILING DATE: 28-July-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: Noland, Greta E.
RECESTRATION NUMBER: 35,302
RECESTRATION NUMBER: 35,302
RECESTRATION NUMBER: 35,302
RECESTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Indels
                                                                                       NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray
Bicknell
            Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
INVENTION: DNA Encoding Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.6%; Score 4474.5; Best Local Similarity 94.7%; Pred. No. 0; Matches 860; Conservative 21; Mismatches
                                                                          Phosphodiesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-697-894-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELEPHONE: (312) 346-5750
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INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
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APPLICANT:
                                                          TITLE OF
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APPLICANT: Filzer Limited
APPLICANT: Maw, Graham Nigel
APPLICANT: Mayman, Christatopher Peter
TITLE REFERENCE: Compounds for the Treatment of Female Sexual Dysfunction
TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
FILE REFERENCE: PC10343B
CURRENT APPLICATION NUMBER: US/10/686,390
CURRENT FILING DATE: 2003-10-15
PRIOR FILING DATE: 2000-01-08
PRIOR FILING DATE: 2000-01-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-15
PRIOR FILING DATE: 2000-07-15
PRIOR FILING DATE: 2000-07-15
PRIOR FILING DATE: 2000-07-15 393 513 613 433 493 553 573 633 673 693 733 753 793 813 853 873 913 874 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGTRAPIN 933 334 PVISRATDQVVALACAFNKLEGDLFTDBDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVDDE HINTO SOBEYTKLIHDGIQPVAAIDSNFASFTYTPRSLPEDDISMAILSMLQDMNFINNYK IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC IDCPTLARFCLMVKKGYRDPPYHNMMARFSVSHFCYLLYKNLELTNYLEDIEIFALFISC 694 MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVWERHHFAQAIAILNTHGCNIFDHFSRKD HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD 754 YORMLDLMRDILLATDLAHHLRIFKDLQKWABVGYDRNNKQHHRLLLCLLMTSCDLSDQT KGWKTTTRKIABLIYKEFFSOGDIBKAMGNRPMEMMDRBKAYIPBLOISFMEHIAMPIYKL **LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN** QALLQVAKNLFTHLDDVSVLLQEI ITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQE VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY YQRMLDLMRDIILATDLAHHLRIPKDLQKWABVGYDRTNKQHHSLLLCLLMTSCDLSDQT KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL

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APPLICANT: Pitzer Limited
APPLICANT: Pitzer Limited
APPLICANT: May, Graham Nigel
APPLICANT: May, Graham Nigel
APPLICANT: Wayman, Christopher Peter
TILE APPLICANT: Wayman, Christopher Peter
TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
FILE REBERENCE: PC10343D
CURRENT APPLICATION NUMBER: US/10/686,282
CURRENT PLING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PLILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR APPLICATION NUMBER: GB 992643.6
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
PRIOR PLILOR DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-13
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; Pred. No. 0;
21; Mismatches
                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10686282; Publication No. US20050020547A1; GENERAL INFORMATION: APPLICANT: Pfizer Inc.
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Matches 860; Conservative
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US-10-686-282-5
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION WUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
LENGTH: 941
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ORGANISM: Homo Sapiens
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94.7%; Pred. No. 0;
ive 21; Mismatches
PRIOR APPLICATION NUMBER: GB 0017141.3
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 5-
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Matches 860; Conservative
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; ORGANISM: Homo Sapiens
US-10-686-349-5
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Sequence 5, Application US/10666349

Publication No. US20050070499A1

GENERAL INFORMATION:

APPLICANT: Pfizer Linc.

APPLICANT: Pfizer Linc.

APPLICANT: Mayman, Christopher Peter

TITE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction

FILE REFERENCE: PC10343C

CURRENT TAPLICATION NUMBER: US/10/686,349

CURRENT TAILNG DATE: 2003-10-15

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-39

PRIOR FILING DATE: 2000-03-39
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                                                                634 IDCPTLARFCLMVKKGYRDPPYHNWHAFSVSHFCYLLYKNLELTNYLEDIEIFALFISC
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QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE
                                                                                                                                   QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGGVVDDE
                                                                                                                                                                                                                                             VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMY
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                                                                                 600 CPILARFCLMVKKGYRDPPYHNMHAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMC
                                                                                                                                                                RMLDLMRDIILATDLAHHLRIFKDLQKWAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKG
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                                                                     CPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMC
                                                                                                                    HDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQ
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                       KVSDDEYTKILHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKID
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US-10-108-260A-2928

; Sequence 2928, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TILE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILID DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SEQ ID NOS: 5458
; SEQ ID NOS: 528
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                                                                                                                                                                       Sequence 4, Application US/10094989;
Publication No. US20020115179A1
GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: PROTEINS, NUCLBIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, NUCLBIC ACID MOLECULES ENCODING HUMAN;
TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF;
FILE REFERENCE: CLOOJO63DIV;
CURRENT PILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR PILING DATE: 2001-01-05
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 4:
LENGTH: 905
300 ISRATDQVVALACAFWKLGGDLFTDEDEHVIQHCFHYTSTVLTSTLAFQKGQKLKCECQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIRIPADGGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                     93.64; Score 4473.5;
larity 94.94; Pred. No. 0;
Conservative 20; Mismatches
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ORGANISM: Homo sapien
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Matches 860; Conserv
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              241 CCLLLVSEDNLQLSCKVIGDKVLGEEVSFPL-TGCLGQVVEDKKSIQLKDLTSEDVQQLQ 299
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                                                     300 SMLGCELQAMLCVPVISRATDQVVALACAFNKLEGDLFTDEDEHVIQHCFHYTSTVLTST
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                                                                                                                                                                                                                                                                                                   420 VAKVFDGGVVDDESYEIRIPADQGIAGHVATTGQIINIFDAYAHPLFYRGVDDSTGFRTR
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                                                                                                               CCLLLVSEDNLQLSCKVIGDKVLEERISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQ
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Job time : 118.692 secs
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                                                                     QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVDDE
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TILE OF INVENTION: No. US20030236392Alel full length cDN;
FILE REFERENCE: H1-A0105;
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25;
FRIOR PEDLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096;
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-104-047-2944
Sequence 2944, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
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Best Local Similarity 93.8
Matches 684; Conservative
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June 26, 2005, 12:06:11; Search time 115.187 Seconds (Without alignments) 3092.423 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-697-894-39

4781 1 MRRQPAASRDLFAQEPVPPG......VPDLDGARAPINGCCSLDAE 921 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Deco4:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:* Database

geneseqp2003as:*geneseqp2003bs:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aar69727 Cyclic-GM	Aaw11252 Clone p3C	Aaw18048 Cyclic-GM	Aaw71224 cGS-PDE e	Aaw77040 Adrenal c	-	Aay80984 Bovine ad	Abu58723 Bovine ad	Adq94959 Bovine p3	CGS-PDI	Aar69728 Cyclic-GM	Aaw11239 Cyclic GM	Aaw18049 cGS-PDE a	Aaw71225 Bovine br	Aaw77041 Cyclic-GM	Aaw60753 cGS-PDE i	Aay80985 Bovine br	Abu58724 Bovine br	Adq94963 Bovine cG	Aar28408 CGS PDE f	Abr54205 Human NOV	Aao15507 Human pho	Abg70998 Human pho	Cyclic	Aaw11253 pHcgs6n c
ΙD	AAR69727	AAW11252	AAW18048	AAW71224	AAW77040	AAW60752	AAY80984	ABU58723	ADQ94959	AAR28407	AAR69728	AAW11239	AAW18049	AAW71225	AAW77041	AAW60753	AAY80985	ABU58724	ADQ94963	AAR28408	ABR54205	AA015507	ABG70998	AAR69729	AAW11253
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Aaw18050 Human cGS Aaw71226 Human cGS Aaw7042 Cyclic-GM Aaw60754 Human cyc Aay80986 Human cGS Aae07954 Human pho Aae07918 Human pho Aab85117 Human pho Aab85106 Human cGM Aab85105 Human cGM Aab85105 Human cGM Aab85105 Human cGM Aab85105 Human cGM	Human Human Human Plasmi Human Rat Pr Human Human
AAW18050 AAW71226 AAW71042 AAW60754 AAX80986 AAX807954 AAB85117 AAB85116 AAB85106 AAG66539	ADD14154 ADG21792 ADG24965 AAR28409 AAR28409 ADB62312 ADM62243 ADB64790 ADR10446
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ALIGNMENTS

Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies; bovine adrenal cortex; hormones; neurotransmitters; transmission regulation; enzyme purification; clone p3CGS-5. Cyclic-GMP stimulated nucleotide PDE clone p3CGS-5. AAR69727 standard; protein; 921 AA (revised)
(first entry) 25-MAR-2003 11-0CT-1995 AAR69727; AAR69727

Bos taurus

US5389527-A.

14-FEB-1995.

92US-00872644. 20-APR-1992;

91US-00688356 19-APR-1991;

(UNIW) UNIV WASHINGTON

Beavo JA; Sonnenburg WK, Charbonneau H,

WPI; 1995-090205/12.

N-PSDB; AAQ83974.

New nucleic acid encoding cyclic-GMP stimulated nucleotide phosphodi:esterase - and related vectors and transformed cells, useful for screening cpds. for phospho-di:esterase modulating activity.

Claim 1; Col 65-74; 69pp; English.

AAQ83974 encodes AAR69727 the bovine adrenal cortex cyclic-GMP stimulated nucleotide phospho-diesterase (CaM PDE) clone p3GCs-5. Eukaryotic cells that express CaM PDE can be used to screen cpds. for the ability to modulate CaM PDE activity. CaM PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other against CaM PDE can be used for enzyme purifen., or determination. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 921 AA;

(first entry)

(revised)

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Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; adrenal gland; cGMP; transmembrane signal; extracellular hormone; neurotransmitter; antibody.
                                                          Clone p3CGS-5 cyclic GMP stimulated phosphodiesterase.
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                                                             MRRQPAASRDLFAQEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETV
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encoding cGMP-stimulated phospho:di:esterase - for prodn.

Beavo JA;

Sonnenburg WK,

94US-00297494 91US-00688356 92US-00872644

taurus.

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This sequence represents the cyclic GMP stimulated phosphodiesterase (CGS -PDE) clone p3CGS-5 isolated from bovine adrenal cortex. The cyclic nucleotide phosphodiesterases (PDEs) catalyse the hydrolysis of 3', 5' cyclic nucleotides, such as cAMP and CGMP, to their corresponding 5'- cyclic nucleotide monophosphates. The PDEs are therefore important in the control of the cellular concentration of cyclic nucleotides. The PDEs control of the cellular concentration of cyclic nucleotides. The PDEs are, in turn, regulated by transmembrane signals or second messenger control in regulating the flow of information from extracollular hormones, concernamitters, or other signals that use the cyclic nucleotides as messengers. PDEs are present in most of the cells and tissues of cutaryotic organisms, but only in trace amounts. CGS-PDEs are stimulated by cGMP in effecting cAMP hydrolysis. This is thought to occur through a concatalytic cGMP-specific site present on the CGS-PDE. The cDNA encoding this sequence can be used for the production of recombinant CGS-PDE, which may have therapeutic and diagnostic uses. This protein may also be cuseful for diagnostic antibody production. (Updated on 25-MAR-2003 to
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iive 0; Mismatches
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Matches 921; Conservative
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RESULT 2 AAW11252 ID AAW11252 standard; protein; 921 AA.

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                                                          SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTST
                                                                                                                                   421 VANVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIFDAYAHPLFYRGVDDSTGFRTR
                                                                                                                                                                    NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
                                                                      SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTST
                                                                                                   QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
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                                                                                                                                                                                                                                     SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNMMHAFSVSHFCYLLYKNLELTNY
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                                                                                           LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL
                                                                                                                          VAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR
                                                                                                                                                          NILCPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
                                                                                                                                                                                                                           SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNY
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The present sequence represents the amino acid sequence from the large open reading frame of p3cGS-5 cDNA bovine adrenal cortex clone insert. The presence of 36 acenosine residues at the 3'-end of the cDNA preceded by a transcription termination consensus sequence suggests that all of the 3' untranslated sequence of the cyclic-GMP-stimulated by phosphodisererase (GGS-PDE) mRNA is represented by this clone. The DNA sequences of the GGS-PDE's are used for the production of the recombinant serzymes, which in turn may be used for antibody production and to screen for compounds that modulate phosphodisererase activity. (Updated on 25-MAR-2003 to correct PI
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                                                                                                        DNA encoding bovine and human phosphodiesterase enzymes - stimulated calcium/calmodulin, useful for recombinant prodn. of the enzymes.
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enzyme;

Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase calcium ion; antibody; cow; polymerase chain reaction.

94US-00297510

29-AUG-1994;

US5602019-A. 11-FEB-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDE; assay; identification; modification; enzymatic activity; modulator; cyclic guanosine monophosphate-stimulated phosphodiesterase; cGS-PDE.
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through pathways involving these, regulate flow of information from extracellular hormones, neurotransmitters and other signals using cyclic nucleotides as messengers. The specification describes an assay for identifying a chemical agent which modifies the enzymatic activity of a mammalian CaM-PDE. The assays are useful for identifying modulators of CAM-PDE with the suspected modulator and measuring cells expressing CAM-PDE with the suspected modulator and measuring its effect e.g. monitoring the hydrolysis of cAMP and/or CGMP
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                                181 APEATQNPPEEAAGDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQYLQOETQASR
                                                                                                                                                                                                          301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTST
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                                                                                                                                                                                                                                                                                                      361 LAPQKEQKLKCECQALLQVAKOLFTHLDDVSVLLQEIITEARNLSNAEICSVPLLDQNEL
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SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
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                                                                                                                                                                                                                                                                                                                                                                                    68; cow; Ca2+ stimulated phosphodiesterase;
Calmodulin stimulated phosphodiesterase; therapeutic; antibody
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                                                                                                                                                                                                                                                                                                                                            cortex Ca2+/calmodulin stimulated phosphodiesterase.
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iive 0; Mismatches
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                                                                      Sonnenburg WK, Charbonneau H,
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92US-00872644.
94US-00297494.
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Matches 921; Conservative
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20-APR-1992;
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                                                                                                                                                                                             OYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
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421 VAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR
                                                                                      NILCFPIKNENOEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
                                                                                                                                                              QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
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                                                       NILCFPIKNENQEVIGVAELVNKINGFWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
                                                                                                                                                                                                                                                                        SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNY
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94US-00297494.
95US-00455525.
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N-PSDB; AAZ90377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New calmodulin and calcium stimulated cyclic nucleotide phosphodiesterase - used e.g to identify selective modulators, potentially useful as e.g. cardiotonic, antidepressant, antihypertensive agents.
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100.0%; Pred. No. 0;
Live 0; Mismatches
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                                                                                                         95US-00479532.
                                                                                                                                                              91US-00688356,
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94US-00297494
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N-PSDB; AAV36153.
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                                                                                                                                                                                       20-APR-1992;
29-AUG-1994;
                                                  07-JUL-1998
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cincoding mammalian Ca2+/Calmodulin-stimulated phosphodiesterases (CaM-PDES) and cyclic guanidine monophosphare (CGMP)-stimulated phosphodiesterases (CGS-PDES). In particular the invention relates to an assay for identifying chemicals that modify the enzymatic activity of a mammalian cGS-PDE. The PDES catalyse the hydrolysis of of cyclic nucleotides to their corresponding 5'-nucleoside monophosphates. In this way they control the cellular concentration of cyclic nucleotides.

Conclections to their corresponding 5'-nucleoside monophosphates. In this way they control the cellular concentration of cyclic nucleotides of neurotransmitters or other signals that use cyclic nucleotides as neurotransmitters or other signals that use cyclic nucleotides as nessengers. The PDES in turn are regulated by transmembrane signals or econd messenger ligands such as Ca2+ or cGMP. Inhibitors of these enzymes are potentially useful as cardiotonics, antidepressants, antidhypertensives or antithrombocics. The method of the invention can identify specific inhibitors of particular isoforms of CGS-PDES.

Cadentify specific inhibitors of particular isoforms of CGS-PDES from bovines
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                   HGCNI FDHFSRKDYQRMLDLMRDI ILATDLAHHLRI FKDLQKMAEVGYDRTNKQHHSLLL
                                                                                   CLLMTSCDLSDQTKGWKTTRKIAELIYKEPPSQGDLEKAMGNRPMEMMDREKAYIPELQI
                                                                  CLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI
                                                                                                                                  SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
                                                                                                                                                   New purified and isolated DNA sequence encoding a mammalian calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide phosphodiesterase polypeptide, useful for therapeutic, diagnostic and prognostic applications.
HGCNI PDHFSRKDYQRMLDLMRDI I LATDLAHHLRI PKDLQKMABVGYDRTNKQHHSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cow; Ca2+/calmodulin stimulated phosphodiesterase; enzyme; CaM-PDB; 59KDa CaM-PDB; 61kDa CaM-PDB; 63kDa CaM-PDB; GCS-PDB; cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent; anti-hypestensive; anti-thrombotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charbonneau H, Sonnenburg WK;
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92US-00872644.
95US-00455526.
98US-00123783.
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used in therapeutic, diagnostic and prognostic applications and in the preparation of antibodies. Isolated chemical agents which are inhibitors of PDEs may have anti-depressant, anti- hypertensive or anti-thrombotic activities or may be cardiotonic agents. The present sequence is a Bovine CaM-PDE or cGS-PDE (or fragment) of the invention
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31-MAY-1995; 95US-00455526.
28-UUL-1998; 98US-00127783.
18-JUN-2001; 2001US-00883825.
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                 DTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSV
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An unamplified bovine adrenal cortex cDNA library was prepd. and screened with redundant 23-mer antisense oligonucleotide probes end labelled with radiolabelled ATP and T4 polynucleotide kinase. A single 2.1 kb cDNA clone (designated pcGS-3:2.1) was obtd. This clone was used to screen a second, amplified bovine adrenal cortex cDNA library to yield 52 putative clones. The largest insert was of 4.2 kb in a plasmid designated p3CGS-5. The cDNA encodes a 921 residue protein with mol. wt. 103 kD. (Updated on 25-MAR-2003 to correct PN field.)
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  QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
           SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWHAFSVSHFCYLLYKNLELTNY
                                                SMLQDMNPINNYKIDCPTLARFCLMVKKGYRDPPYHWMHAFSVSHFCYLLYKNLELTNY
                                                                            LEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNT
                                                                                      LEDMEIFALFISSMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVWERHFFAQAIAILNT
                                                                                                                  HGCNI FDHFSRKDYQRMLDLMRDI I LATDLAHHLRI FKDLQKMAEVGYDRTNKQHHSLLL
                                                                                                                            CLLMTSCDLSDQTKGWKTTRKIAELIYKBFFSQGDLEKAMGNRPMEMMDREKAYIPELQI
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215 GDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL 274
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134 AGAVAAVILVHCGQLSDNEEWSLQAVERHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                        155 AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                         GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
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                                                                                                                                                                                                                                                                             PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW18049 standard; protein; 942 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 QEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKRALSAVLPKVETVYTYLLDGESRLVC 73
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                                                                                                                                                                                                                                                                        Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP; adrenal gland; cGMP; transmembrane signal; extracellular hormone; neurotransmitter; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beavo JA;
                                                                                                                                                                                                                             Cyclic GMP stimulated phosphodiesterase.
                                                               AAW11239 standard; protein; 942 AA.
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92US-00872644.
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Best Local Si
Matches 898;
                                                                                                          AAW11239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDE; assay; identification; modification; enzymatic activity; modulator; cyclic guanosine monophosphate-stimulated phosphodiesterase; CGS-PDE.
                                                                           HWKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                            LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN
                                                                                                                                                                                                                                                                                              755 YQRMLDLMRDIILATDLAHHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQT
                                                                                                                                                                                                                                                                                                                                                                                                                     LODLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN
HMKVSDDEYTKLLHDGIQPVAAIDSNPASFTYTPRSLPEDDTSMAILSMLQDMNPINNYK
                                                                                                                            IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC
                                                                                                                                                                635 IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHPCYLLYKNLELTNYLEDMEIFALFISC
                                                                                                                                                                                                    MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD
                                                                                                                                                                                                                                        MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD
                                                                                                                                                                                                                                                                          YQRMLDLMRDIILATDLAHHLRIFKDLQKWAEVGYDRTNKQHHSLLLCLLMTSCDLSDQT
                                                                                                                                                                                                                                                                                                                                               KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine brain cGS-PDE segeunce of clone pBBCGSPDE-7.
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GCCSLDAE 942
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                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence. The large open reading frame encodes a 942-residue polypeptide that is nearly identical to the adrenal gland cyclic-GMP-stimulated phosphodiesterase (GGS-PDE) isozyme. The difference in the primary structure of the two isozymes lies in the amino-terminal residues 1-46 of the brain cGS-PDE, and residues 1-25 of the adrenal cGS-PDE. The remaining carboxy-terminal residues in both are identical. The DNA sequences of the cGS-PDE's are used for the production of the recombinant enzymes, which in turn may be used for antibody production and to screen for compounds that modulate phosphodiesterase activity. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQYLQGETQASRCCLLLVSEDNLQL 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDOKGGVAYTNODRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL 253
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                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents the pBBCGSPDE-7 bovine brain insert amino
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                                                                                                                                                                                                        Beavo JA;
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                                                                                                                                                                                                      Bentley JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 4657; DE
; Pred. No. 0;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 5; Col 85-92; 69pp; English.
                                                                                                                                                                                                      Charbonneau H,
                                                                           94US-00297510
                                                                                                           91US-00688356.
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Best Local Similarity 98.9
Warrhes 898; Conservative
                                                                                                                                                                (UNIW ) UNIV WASHINGTON
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                                                                                                                                                                                                                                                          N-PSDB; AAT67223.
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                                                                                                                                                                                                      Sonnenburg WK,
                                                                                                                                20-APR-1992;
   US5602019-A.
                                                                                                             19-APR-1991
                                       11-FEB-1997
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29-AUG-1994;
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Calmodulin a
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monophosphate-stimulated phosphodiesterase (cGS-PDE) cDNA. The specification also describes Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase (Cam-PDE) enzymes. Cam-PDE argymes catalyse the hyposphodiesterase (Cam-PDE) enzymes as as used catalyse the hydrolysis of cyclic nucleotides and as such control their intracellular level. They are controlled by second messengers e.g. Ca2+ and calmodulin and transmembrane signals and through pathways involving these, regulate flow of information from extracellular hormones, neurotransmitters and other signals using cyclic nucleotides as messengers. The specification describes an assay for identifying a chemical agent which modifies the argymatic activity of a mammalian CaM-PDE. The assays are useful for identifying modulators of CaM-PDEs. The assays are useful for incubating cells expressing CaM-PDE with the suspected modulator and messuring its effect e.g. monitoring the hydrolysis of CAMP and/or CGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE 133
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98.9%;
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EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cyclic-GMP-stimulated phosphodiesterase clone pBBCGSPDE-7 from the
                                                                               LODLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN
KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine brain, is one of several phosphodiseterases isolated in this invention. The phosphodiseterases were used to transform host cells, preferably mammalian or yeast cells. The recombinant proteins and fragments produced can be used for therapeutic, diagnostic, and prognostic purposes and will provide the basis for preparation of monoclonal and polyclonal antibodies. An antibody specific for the cat, foalmodulin-stimulated cyclic nucleotide phosphodiseterase (PDE) polypeptide is useful for affinity purification or detection of the plypeptide and is selective only for the Ca2+/calmodulin stimulated cyclic nucleotide PDE polypeptide.
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stimulated phosphodiesterase; therapeutic; antibody.
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                             standard; protein; 942 AA.
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                                                                                                                                                                                                                                                                                                                                                      MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD 733
                                                                                                                                                                                                                                                                                                                                                                                         YQRMLDLMRDIILATDLAHHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQT 793
EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE 154
                                                                                                                                                                 SYEIRIPADQGIAGHVATTGQILNIPDAXAHPLFYRGVDDSTGFRTRNILCFPIKNENQE
                            AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                                                            PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC
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                  AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                      GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
                                                               SCKVIGDKVLEERISPPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV
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Search completed: June 26, 2005, 12:17:19 Job time : 121.187 secs

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Comment=Additional isoforms seem to exist;
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421 VAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR
                                                                                     QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL
                                                                                                                                                                                                      SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWHAFSVSHFCYLLYKNLBLTNY
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                                                                      NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM PDE2A3).
TISSUE=Fetal brain, and Hippocampus;
MEDLINE=97354299; Pubmed=9210593; DOI=10.1016/S0378-1119(97)00046-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
55-JUL-2004 (Rel. 44, Last annotation update)
cGMP-dependent 3',5'-cyclic phosphodiesterase (RC 3.1.4.17) (Cyclic
GMP stimulated phosphodiesterase) (CGS-PDE) (cGSPDE).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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IsoId=O00408-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Catalytic.
Nacetylmethionine.
MRACPAASTDLFAGEPVPFGSGDGA -> MGQACGHSILCR
SQQYPAARPAREPREGQVFLKPDEPPPPPPPPPQFGADS (in
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                                                                                                                                                                                                                                                                                                                                                                                                                         cGMP; Direct protein sequencing;
                                                      IsoId=Pl4699-2; Sequence=VSP 004555;
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 4781; DB 1; Length 921; 100.0%; Pred. No. 1.3e-278; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 004555.
N -> D (in Ref. 2).
P -> L (in Ref. 4).
V; E29F4C9875E83640 CRC64;
             Name=PDE2A2;
ISOId=P14099-3; Sequence=Not described;
IsoId=P14099-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                       PIR, A40981, A40981.
InterPro; IPR003018; GAF.
InterPro; IPR003067; Met phos hydro.
InterPro; IPR002073; PDEase.
Pfam; PF0023; PDEase I; 1.
PRINTS; PR0023; PDESE I; 1.
SWART; SM00065; GAF; 2.
SWART; SM00471; HDC; 1.
                                                                                                   SIMILARITY: Contains 1 GAF domain.
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Acetylation; Alternative splicing;
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633 633 P
921 AA; 103227 MW;
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EMBL; L49503; AAA87353.1; -.
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Best Local Similarity 100.
Matches 921; Conservative
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                                        Name=PDE2A3;
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                                                                                                                                                                                                        IDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC
                                                                                                                                                                                                                                                                                                                                             MCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKD
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                                                                HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCKVIGDKVLGEEVSFPL-TGCLGQVVEDKKSIQLKDLTSEDVQQLQSMLGCELQAMLCV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 PVISRATDQVVALACAFNKLEGDLFTDEDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCEC 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004118; F:cGMP-stimulated cyclic-nucleotide phosphodi. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALRRVQVLQQRGPREAPRAVQNPPEGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 QEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTYLLDGESRLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPPPPPQPCADSLQDALLSLGSVIDISGLQRAVKEALSAVLPRVETVYTYLLDGESQLVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLEYRGVDDSTGRRTRNILCFPIKNENQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            891 Catalytic (By similarity).
105716 MW; 9797609B487FD64E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003018; GAR.
InterPro; IPR0030018; Met_phos_hydro.
InterPro; IPR0030018; Met_phos_hydro.
InterPro; IPR002013; PDEase.
Pfam; PP01559; GAR; 2.
Pfam; PP00233; PDEase I; 1.
PRINTS; PR00387; PDIESTERASE1.
SWART; SW000471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
PROSITE; PS00126; PDEASE I; 1.
Alternative splicing; CGMP; Hydrolase; Membrane.
DOMAIN 633 891 Catalytic (By similari;
IsoId=000408-2; Sequence=Not described;
                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 GAF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67733; AACS1320.1; -. Genew; HGNC:8777; PDE2A.
MIM; 602658; -.
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                                Name-PDE2A2
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                                                                                                                                                                                      QEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTYLLDGESRLVC
                                                                                                                                                                                                                                       GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSBDNLQL
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                                                                                                                                                                    Gaps
R EMBL; BC040974; AAH40974.1; -..
R GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a...
R GO; GO:000314; F:atalytic activity; IEA.
R GO; GO:0007165; P:eignal transduction; IEA.
R InterPro; IPR003018; GAF.
R InterPro; IPR00307; Met phos_hydro.
R InterPro; IPR00307; Met phos_hydro.
R InterPro; IPR00307; PDEase.
R Ffam; PF00129; PDEase.
R Ffam; PF00129; PDEase I; 1.
R PRINTS; PR00387; PDIESEI.
R SWART; SM0065; GAF; 2.
SWART; SM00671; HDc; 1.
                                                                                                                                                                  1;
                                                                                                                                                DB 2; Length 941;
                                                                                                                                              Query Match 93.4%; Score 4466.5; DB 2; Length Best Local Similarity 94.5%; Pred. No. 1.1e-259; Matches 858; Conservative 22; Mismatches 27; Indels
                                                                                                                   PS00126; PDEASE I; 1.
941 AA; 105648 MW; 93028FC28CB54D6B CRC64;
                                                                                                                   PROSITE; 1
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 KGWKTTRKIABLIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPBLQISFMEHIAMPIYKL
                                                 LODLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (2.86 ANGSTROMS) OF 183-549 IN COMPLEX WITH GMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMP (cGMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The two GAF domains in phosphodiesterase 2A have distinct roles in
                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 3.1.4.17) (Cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iby smilatity).
-!- CATALYTIC TYSTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O
nucleoside 5'-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Turley S.,
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                                                                                                                                                                                                                                                                                                                             092254; Q8K2U1;
28-FEB-2003 (Rel. 41, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
CGMP-dependent 3,5'-cyclic phosphodiesterase (EC 3...
GMP stimulated phosphodiesterase) (CGS-PDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dimerization and in cGMP binding.";
Proc. Natl. Acad. Sci. U.S.A. 99:13260-13265(2002).
-!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12271124; DOI=10.1073/pnas.192374899;
Martinez S.E., Wu A.Y., Glavas N.A., Tang X.-B.,
Hol W.G.J., Beavo J.A.;
                                                                                                                                                                                                                                                                                                            916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                            GCCSLDAE 921
                                                                                                                                                                                      GCCSLDAE 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               900
                                                                                                                                               CLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMDREKAYIPELQI
                                                                                                                                                                                                                                                                                                                                           837 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
                                                                                                                                                                                                                                                                               841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY
HGCNI FDHFSRKDYQRMLDLMRDI ILATDLAHHLRI FKDLQKMABVGYDRNNRQHHRLLL
                                                                                             CLLMTSCDLSDQTKGWKTTRK1AEL1YKEFFSQGDLEKAMGNRPMEMMDREKAY1PEL01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CGMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
GMP stimulated phosphodiesterase) (CGS-PDE) (cGSPDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley, TISSUE-Brain;
MEDLINE=95110334; PubMed=7811274;
Yang Q., Paskind M., Bolger G., Thompson W.J., Repaske D.R.,
Cutler L.S., Epstein P.M.
"A novel cyclic GMP stimulated phosphodiesterase from rat brain.";
Biochem. Biophys. Res. Commun. 205:1850-1858(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92406782; PubMed=132632;
Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;
"A polymerase caracion strategy to identify and clone cyclic nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA encoding the 63-kDa calmodulin-dependent phosphodiesterase.";
J. Biol. Chem. 267:18683-18688(1992).
-I- FUNCTION: Hydrolyzes both cyclic AMP (CAMP) and cyclic GMP (CGM-1-FUNCTION: Hydrolyzes both cyclic AMP (CAMP) and cyclic GMP (CGM-1-CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=Q01062-3; Sequence=Not described;
TISSUE SPECIFICITY: Brain.
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Experimental
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-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist. Exp
confirmation may be lacking for some isoforms
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802

854

922

914

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CTISSUB-Adrenal gland;

Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

A Wakebe H., Ono T., Hishigaki H., Watanabe T., Osaki K., Sugiyama T.,

Trie R., Otsuki T., Sato H., Ota T., Wakamatu A., Ishii S.,

A ramamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

Ximura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,

Xikuchi H., Kanda K., Wagatsuma M., Kawakami B.,

Xikuchi H., Kanda K., Wagatsuma M., Kawakami B.,

Xibunitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

Sugano S., Nagahari K., Setilo-nucleotide phosphodiesterase a. .; IEA.

GO; GO:0001165; P:signal transduction; IEA.

InterPro; IPR003018; GAF.

InterPro; IPR003018; GAF.

InterPro; IPR003013; PDEase.

DR Pfam; PP01233; PDEase.

PFam; PP00233; PDEase.

PFam; PF00233; PDEase.
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QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPING
                                                                                            GWKTTRKIAELIYKBPPSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16750.
Hypothetical protein FLJ16750.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 250;
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SEQUENCE 685 AA; 78177 MW; A6087394B98221C3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 AA
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SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
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Matches 637; Conservative
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Q6ZMR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOKDEKGYTAHDRKILQLCGELYDLDATSLQLKVLRYLQQETQATHCCLLLVSEDNLQLS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 735 QRMLDLMRDIILATDLAHHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTK 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 VISRATDQVVALACAFNKLGGDFFTDEDERAIQHCFHYTGTVLTSTLAFQKEQKLKCECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVDDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VISRATDOVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCM
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 879 Catalytic (By similarity).
646 646 W - R (In Ref. 2).
758 L -> M (In Ref. 2).
928 AA; 104663 MW; EF0B8CIE266EAB18 CRC64;
EMBL; U21101; AAA63683.1; -.
EMBL; M94540; AAA60922.1; -.
PIR; JC2486; JC2486.
RGD; 620965; PG248.
InterPro; IPR003018; GAF.
InterPro; IPR0030018; GAF.
InterPro; IPR003003; MeL_phos_hydro.
InterPro; IPR003003; MeL_phos_hydro.
InterPro; IPR0030303; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase.
SMART; SM00065; GAF; 3.
SMART; SM00471; HD.5; 1.
PROSITER; PS00126; PDEASE I; 1.
PROSITER; PS00126; PDEASE I; 1.
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003018; GAF.
InterPro; IPR003018; GAF.
InterPro; IPR002073; PDEase.
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                            SCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV
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                                                                                                                                 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
EPPDE2.
Ephydatia fluviatilis.
Ephydatia, Metazoa, Porifera, Demospongiae, Ceractinomorpha, Haplosclerida, Spongillidae, Ephydatia.
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                                                                                               |::|| |::| | ::: |: | | ::|| TYNGVPLDKEIRKPVSSSIYGECFTTGEIINISNV-PQDMRFNPRIDTIKGYEPTHLLCI
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238

82 82 548

608 536

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LCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLK 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :: |: | | | | : : : | : : : |: | : : | : : | : : | : : | : : | : : | : | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CECCALLOVAKNLFTHLDDVSVLLOEIITEARNLSNAEICSVFLLDQNE--LVAKVFD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker S.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; ANIZ2262, AAM52774.1; ...
FlyBase; FBgn0032686; PGel1.
GO; GO:000414; F:3',5'-cyclic-nucleotide phosphodiesterase a...
GO; GO:000165; P:signal transduction; IEA.
InterPro; IPR003018; GAF.
InterPro; IPR003018; Met_phos_hydro.
InterPro; IPR002013; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise J
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.
                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE 1544 AA; 171689 MW; F5254E0CCDB3D065 CRC64;
                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%; Score 992; DB 2; L. L. L. 32.2%; Pred. No. 1.4e-50; Conservative 147; Mismatches 302;
                                                                                                                                                                                                      PRT; 1544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDBase I; 1.
PRINTE; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                      Name=Pde11; Synonyms=CG10231;
                                               878
                                                                                         477 FLDTIDŠNŘÉQWERV 491
                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                               864 LYERVASNREHWTKV
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGI 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILATDLAHHLRIFKDLQKM-AEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKGYRDPPYHNWMHAFSVSHFCYLLYKNLEL--TNYLEDMEIFALFISCMCHDLDHRGTN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDI 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPVAAIDS---NFASFTYTPRSLPEDDTSMAI-LSMLQDMNFINNYKIDCPTLARFCLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AAAB01008964; EAA12229.1; -.
GO; GO:0004114; F:3'.5'-cyclic-nucleotide phosphodiesterase a.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003018; GAF.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.9%; Score 1236; DB 2; Length 491; 50.5%; Pred. No. 5.8e-66; tive 91; Mismatches 138; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 AA; 56349 MW; 5416132C4CE42EF3 CRC64;
                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           Name=ebiG6713; ORFNames=ENSANGG0000005075;
Anopheles gambiae str. PEST.
                                                                                                                                                             491
      PIYKLLQDLFPKAAELYERVASNREHW
                                             PVYOLLSRLLPESAAAYHTLLDNREQW
                                                                                                                                                                                                      Created)
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 1.
Pfam; PF00213; PDEase I; 1.
PRINTS; PR00387; PDIESTERASEI.
PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                             ul-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, EbiP6713 (Fragment)
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hes 250; Conserv
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                                                                                                                                                                                                                                                                                        PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 934 AA; 104810 MW; 994675824259447E CRC64;
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AB048417; BAB62712.1; JOINED.
AB048418; BAB62712.1; JOINED.
AB048419; BAB62712.1; JOINED.
AB048420; BAB62712.1; JOINED.
AB048421; BAB62712.1; JOINED.
AB048421; BAB62712.1; JOINED.
                                                                                                                            GO; GO:0004112; F:cyclic-nucleotide
InterPro; IPR003018; GAF.
InterPro; IPR003607; Met_phos_hydro.
InterPro; IPR0032073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase_I; 1.
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PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM004711; HDC; 1.
PROSITE:
                                                                                                           Genew; HGNC:8773; PDE11A.
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                                         | : |: || : || | | AMAKQSYTLEVLSYHASATMDEAHRLRR--LRVPSAVHFRLHDFKFDDIHFEDDDTLKAC 914
                                                                                                                MEDLINE=20469516; PubMed=10906126; DOI=10.1074/jbc.M003041200;
Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
"Isolation and characterization of two novel phosphodiesterase PDE11A variants showing unique structure and tissue-specific expression.";
J. Biol. Chem. 275:31469-31479(2000).
                                                                                        LSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYKNLELTN
                                                                                                                                                              660 YLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQALAILN
                                                                                                                                                                                                                                     THGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD----LQKMAEVGYDRTNKQH
                                                                                                                                                                                                                                                          SPGNQILANLSSDDYCRVIRVLEDAILSTDLAVY---FKKRGPFLESVSQPTSYWVAEEP
                    AQYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAI
                                                                                                                                                                                                                                                                                                             HSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGN-RPMEMMDREKA-
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MEDLINE=20570133; PubMed=11121118;
Yuasa K., Kanoh Y., Okumura K., Omori K.;
"Genomic organization of the human phosphodiesterase PDE11A gene:
"Genomic organizations with other PDEs containing GAF domains.";
Evolutionary relatedness with other PDEs containing GAF domains.";
Eur. J. Biochem. 268:168-178(2001).
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Catarrhini; Hominidae;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphodiesterase 11A (Phosphodiesterase 11A4).
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BAB62712.1; JOINED.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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EMBL; AB036704; BAB16371.1;
EMBL; AB048423; BAB62712.1;
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BAB62712.1;
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AB048409;
AB048410;
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AB048416;
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                                                                                                                                     DRRFNDEIDKLTGYKTKSLLCMPI--RSSDGBIIGVAQAINKIPBGAPFTEDDEKVMQMY
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                                                                                                           EDM--QQLQSMLGCEVQAMLCVPVISRATD-QVVALACAFNKL-GGDLFTDQDEHVIQHC
                                                                                                                                                                                                                                                 : ::: | :| :| | :| | :| | 417 LPFCGIAISNAQLPAASRKEYERSRALLEEVNDLFBEGTDLEKIVKKIMHRAQTLLKCER
                                                                                                                                                                                                                                                                                                                          CSVFLLDQNELVAKVFDGGVVEDESYEIRIP--------ADQGIA
                                                                                                                                                                                                                                                                                                                                                                                CSVLLLEDIESPVVKF-----TKSPELMSPKCSADAENSFKESMEKSSYSDWLINNSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                         447 GHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKING
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY058470; AAL13699.1; --
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Name=Pde6; Synonyma=CG8279;
Drosophila melanogaeter (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
  250 NLQLSCKVIGDKVLE-
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  831 AELVTSEFFEGGDRERLELKLTPSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVK 890
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Mada K., Kanoh Y., Okumura K., Omori K.;
"Genomic organization of the human phosphodiesterase PDB11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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.larity 30.8%; Pred. No. 8.4e-51;
Conservative 159; Mismatches 321; Indels
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Last annotation update)
                                                                                       :: | |:| | :: | ::| |::| 891 LKPMLDSVATNRSKWEELHQKRLLASTASSSS 922
                                                        AAELYERVASNREHWTKVSHKFTIRGLPSNNS 892
                                                                                                                                                                                                                                                   988 AA
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EMBL, AB04842; BAB62713.1; --
EMBL, AB048402; BAB62713.1; JOINED.
EMBL, AB048403; BAB62713.1; JOINED.
EMBL, AB048404; BAB62713.1; JOINED.
EMBL, AB048405; BAB62713.1; JOINED.
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SEQUENCE 988 AA, 111169 MW;
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Pfam; PF00233; PDEase I; 1.
PRINTS; PR00387; PDIESTERASE1.
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BAB62713.1;
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BAB62713.1;
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SMART; SM00471; HDC; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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AB048408; 1
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AB048419; 1
AB048420; 1
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AB048410;
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                                                                                                                                                                                                                                                                                  115 SASSLPEČRRHIMDLDEGELFMELIRDVANELDIDVLCHKILVNVGLLTHADRGSLFLAK 174
                                                                                                                                                                                                                                                                                                         247 -SEDNLQLSCKV-----IGDKVLE---ERISFPLITGRLGQVVEDKKSIQLKDLTSE 294
                                                                                                                                                                                                                                                                                                                                                      295 DMQQLQSMLGCEV-----QAMLCVPVISRATDQVVALACAFNKLGGDL-FTDQDEHV 345
                                                                                                                                                                                                                                                                                                                                                                                                   346 IQHCFHYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                              406 NAEICSVFLLDQN-----ELVAKV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 QAANVSRPSVSELSSSTLAQIAQFVÄTTGQTVNICDV-----IEWVRDHNQIRAEDEID 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 -TRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKV 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 CKLMAKQKVALBCLSYHATASQDQTEKLTQDVI--AEAESYNLYSFTFTDFBLVDDDTCR 579
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            IEA
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                                                                                                                                                                                            Gaps
                                                                                                                                                                   Query Match 20.7%; Score 991; DB 2; Length 1018; Best Local Similarity 30.4%; Pred. No. 8.8e-51; Matches 264; Conservative 150; Mismatches 327; Indels 126;
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       GO; GO: 0001824; F: 75. Tectoride phosphodiesterase GO; GO: 0001824; F: Catalytic activity; IEA.
GO; GO: 0007185; P: Signal transduction; IEA.
InterPro; IPR00318; GAF.
InterPro; IPR00318; GAF.
InterPro; IPR00307; Met_phos_hydro.
InterPro; IPR00307; Met_phos_hydro.
InterPro; IPR00307; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00333; PDEase I; 1.
PRINTS; PR000387; PDESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDc; 1.
                                                                                                                                  PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;
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918 LPKMQVGFIDVICLPLYRVLCDTFPWITPLYEGTLENRRNWQDLAEKVEM-GLTWIDHDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endoptery, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI TaxID=7227;
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Last sequence update)
Last annotation update)
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                                                                                                                                      : | | | | : | : | : | : | : | IDKPVEEFAACADEEIKDIEFTVTTLN
                                                                                LDFLDEEY-----EVPDLDGARAPIN
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                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
MEDLINE=22426065;
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Name=Pde6;
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161 KCERCSVFLVDLDCCEASHLEKIIEKPNQPATRAIKSADSFEEKKWRNRFTVLFELGGEY
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Name=Pde11; ORFNames=CG10231;
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                                                                                          "The transposable elements of the Drosophila melanogaster euchromatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                       MEDLINE=22426069; PubMed=12537572;
Maisra S., Crosby M.A., Mingall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                       Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas Patel S., Frise E., Meler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a
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PlyBase; FB9n0038237; Pe66.
GO; GO:0004114; F:31',5'-cyclic-nucleotide phosphodiesterase (GO; GO:0004114; F:atalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003018; GAP.
InterPro; IPR003073; PDEase.
Pfam; PF00159; GAP; -...
Pfam; PF00159; GAP; -...
Pfam; PF00159; PDEASE.I.
PRINTS; PR00317; PDEESTERASEI.
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SMART; SM00471; HDC; 1.
PROSITE; P00126; PDEASE I; 1.
SEQUENCE 1131 AA; 125538 MW; E63183B04E5FF08A CRC64;
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 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002)
                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
                                                                                                                                                                                                                                                                                          Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%; Score 991; DB 2
30.4%; Pred. No. 1e-50;
                                      MEDLINE=22426070; PubMed=12537573;
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Submitted (MAR-2004)
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MEDINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celliker S.E., Holt R.A., Evana C.A., Gocayne J.D., Adams M.D., Celliker S.E., Holt R.A., Evana C.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brand O.K., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bancos P.V., Berman B.P., Bhandari D., Bolshakov S., Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Davies P., Dorkov B.C., Dunn P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Abrolin K.J. Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W., Roller C., Gabriellian A.E., Garg N.S., Gelbart W., Glasser K.,
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                                                                             521 QAANVSRPSVSELSSSTLAQIAQFVATTGOTVNICDV----IEWVRDHNQIRAEDEID
                                                                                                                                                          -TRNILCPPIKNENOEVIGVAELVNKINGPWFSKPDEDLATAFSIYCGISIAHSLLYKKV
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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IDKPVEEFAACADEEIKDIEFTVTTLN 1016
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Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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InterPro; IPR003018; GAF.
InterPro; IPR003607; Met_phos_hydro.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
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MEDLINE=22426065; PubMed=12537568;
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PRINTS; PR00387; PDIESTERASE1.
SMART; SW00065; GAF; 2.
SMART; SW00471; HDC; 1.
PROSITS; PO0126; PDEASE I; 1.
SEQUENCE 1365 AA; 151173 MW; B0562EFDF5012E56 CRC64;
                                                                                                                                            (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
                                                                                                                       20.6%; Score 983; DB 2; 31.3%; Pred. No. 4.1e-50;
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MEDLINE=2133948; PubMed=11502204;

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Tidentification of rat cyclic nuclectide phosphodiesterase 11A

"Identification of rat and human PDE11A splicing variants.";

"Identification of rat and human PDE11A splicing variants.";

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                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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20.5%; Score 979; DB 2; Length 93:
Best Local Similarity 30.9%; Pred. No. 4.1e-50;
Matches 248; Conservative 157; Mismatches 312; Indels
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935 AA; 104570 MW; B80F1039770F8276 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphodiesterase 11A4.
Name=RNPDE11A4;
                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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Search completed: June 26, 2005, 12:21:45 Job time : 134.535 secs

889 AKLKPMLDSVAANRRKWEELHQK 911

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 26, 2005, 12:09:51; Search time 31.6393 Seconds (without alignments) 2800.810 Million cell updates/sec Run on:

US-10-697-894-39 4781 1 MRRQPAASRDLFAQEPVPPG.......VPDLDGARAPINGCCSLDAE 921 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3',5'-cyclic-nucle	3',5'-cyclic-nucle	protein R08D7.6 [i	probable 3',5'-cyc	3',5'-cyclic-GMP p	3',5'-cyclic-GMP p	'-cyclic-	•	3',5'-cyclic-GMP p	,5'-cyclic-	'-cyclic-	3',5'-cyclic-GMP p	'-cyclic-	'-cyclic-	,5'-cyclic-	,5'-cyclic-		hypothetical prote	adenylate cyclase	ል	3',5'-cyclic-nucle	3',5'-cyclic-nucle	hypothetical prote	3',5'-cyclic-nucle	ņí	3',5'-cyclic-nucle	3',5'-cyclic-nucle	cAMP phosphodieste	cyclic-AMP phospho
SUMMARIES	αi	A40981	JC2486	D88544	S24462	A42828	JW0106	A36617	150186	A47451	S30762	A48719	A34810	JC4520	S13032	S06418	813030	B34611	T25590	AC2089	T24459	871626	161358	T16769	B53109	161259	A54442	I67945	159143	A40949
	Length DB	921 1							862 2													712 2					96	36	~	64
de	Query Match L	100.0	90.5	19.6	19.6	•	16.8		•	16.7	16.5	ė	16.4	15.9	Š.	•	ŝ	15.2		•		8.0	٠				9.0			
	Score	4	4324.5	938.5	938	819.5	801	799.5	799.5	799	791	789	186	758.5	756	754.5	741.5	726	969	404	90	383.5	82.	81.	80	8	8	79	379	379
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Gaps

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Query Match 100.0%; Score 4781; DB 1; Length 921; Best Local Similarity 100.0%; Pred. No. 2e-304; Matches 921; Conservative 0; Mismatches 0; Indels 0

ALIGNMENTS

RESULT 1
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine N;Alternate names: cGMP-dependent phosphodiesterase
C.Species: Bos pinmigenius Cautus (Cattie) C.Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004 C.Accession: A40981; B36112; A36112; B26650; A60179; C26650 R:Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.
J. Biol. Chem. 266, 17655-17661, 1991 A;Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiestera A;Reference number: A40981; MUID:91373395; PMID:1654333
A; Accession: A40981 A; Molecule type: MRNA
A; Cross.references: UNIPROT: P14099, GB: M73512; NID: g162829; PIDN: AAA74559.1; PID: g162839 R; Le Trong, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Ch
HIOCREMISTRY 29, 10280-10288, 1990 A; Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodies. A; Reference number: A36112; MUID:91104948; PMID:2176866
 A;Accession: B30112 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 592-921 <let> A;Accession: A36112</let>
A;Molecule type: protein A;Molecule type: protein A;Residues: 1-203,'D','205-477,'Q','479-921 <let2> A;Residues: 1-203,'D','205-477,'Q','479-921 <let2> R;Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986 A;Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterase A;Reference number: A26650, MUID:87092242; PMID:3025833 A;Accession: B26650</let2></let2>
 A; Molecule type: protein A; Molecule type: protein A; Residues: 613-632, L', 634-794; 808-868 < CHA> A; Residues: 613-632, L', 634-794; 808-868 < CHA> A; Residues: 613-632, L', 634-794; 808-868 < CHA> B; Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Murashima, S.; Manganiel R; Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Murashima, S.; Manganiel Second Messengers Phosphoproteins 13, 87-98, 1991 A; Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-scherence number: Aconseion: Ac
A;Status: not compared with conceptual translation A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Mosicule type: mRNA A;Note: part of this sequence was confirmed by protein sequencing C;Comment: This protein is not glycosylated. C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, CGMP-stimulated; 3',5'-cyclic C;Reywords: accetylated amino end; alternative splicing; cAMP binding; cGMP binding; home P;635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <cnpd> F;1/Modified site: acctylated amino end (Met) #status experimental</cnpd>

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         YTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAP

                                                                               DTQVLVI PLVDKEAGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSV
                                                                                          DTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSV
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                                                                                                                                   APEATQNPPEEAAGDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASR
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JC2486
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - 1
N;Alternate names: cGMP-dependent phosphodiesterase
C;Species: Rattus norvegicus (Norway rat)
C;Date: Z5-Aug.1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C;Accession: JC2486

R;Yang, Q.; Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstel. Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994
A;Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.
A;Reference number: JC2486; MUID:95110334; PMID:7811274
A;Accession: JC2486
A;Molecule type: mRNA
A;Residues: 1-928 «YAN»
A;Coss-references: UNIPROT:Q01062; GB:U21101; NID:g706929; PIDN:AAA63683.1; PID:g706930
A;Experimental source: brain
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, CGMP-stimulated; 3',5'-cyclic-C;Keywords: alternative splicing; cAMP binding; CGMP binding; homodimer; phosphoprotein; P;643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology «CNPD»
F;109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted GAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAAG DQKGGVAYTNQDRK1LQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQLS CKVIGDKVLEEEISPPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCVP CKVIGEKVLGEEVSFPLTMGRLGQVVBDKQCIQLKDLTSDDVQQLQNMLGCELRAMLCVP ALLQVAKNLFTHLDDVSVILQEIITEARNLSNAEICSVFILDQNELVAKVFDGGVVDDES YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFFIKNENGSV DCPTLARFCLMVKKGYRDPPYHNWHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCM GWKTTRKIAELIYKEPPSQGDLEKAMGNRPMEMMDREKAYIPELQISPMEHIAMPIYKLL ALLQVAKNLFTHLDDVSVLLQEIITBARNLSNAEICSVFLLDQNELVAKVFDGGVVEDES YBIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEV MKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKI CHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDY QRMLDLMRDIILATDLAHHLRIPKDLQKWABVGYDRTNKQHHSLLLCLLMTSCDLSDQTK Gaps 5; Query Match
90.5%; Score 4324.5; DB 1; Length 928;
Best Local Similarity 91.7%; Pred. No. 1.4e-274;
Matches 930; Conservative 32; Mismatches 38; Indels 5; ద g 8 8 8 8 요 a 8 6 8 8 8 임 셤 임 ŝ 음 장 ઠે ઠે 8 8 ò ૅ

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probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) ROBD7.6 - Caenorhabdit1 NiAlternate names: hypothetical protein ROBD7.6 (Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 26-Aug-1999 #text_change 09-Jul-2004 C;Accession: 841041; 824462 R;Ainscough, R.; Hawkins, T. Submitted to the EMBL Data Library, May 1992 A;Reference number: 841036 A;Accession: 841041 A;Reference number: 841036 A;Accession: 841041 A;Residues: 1-841 <AIN> A;Residues: 1-841 <AIN> A;Residues: 1-841 <AIN> A;Residues: Thomas K.; Willson, R.; Hillier, L.; Staden, R.; Halloran, N.; Grawkins, T.; Ainscough, R.; Waterston, R.; Millier, L.; Staden, R.; Halloran, N.; A;Aliscough, R.; Waterston, R.; A;Aliscough, R.; Waterston, R.; A;Aliscough, R.; Waterston, R.; A;Aliscough, R.; MulD:92168156; PMID:1538779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aintrons: 31/1; 97/3; 179/2; 260/1; 296/3; 324/3; 622/2; 701/3; 775/3
(Superfamily: Genorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase R08D7.±
C;Keywords: phosphoric diester hydrolaes
F;403-627/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 IFDQFLC-----LTMNL------SALISCIIAEAKKNTEAEDYAVFLHDEDNKQMVL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --NE---LVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVD 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FINETMLATGKKFDMG-----YGIVGKVASTWRTWNIRDVSRCPFFNEID 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYKKVNBAQYRSHLANBMMY--HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSL 590
AS--KSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILA
                                                                                                                                                                                                     748 TDLAHHLRIPKDLQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIY
                                                                                                                                                                                                                                                                                                                            808 KEFFSOGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYER
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19.6%; Score 938; DB 1; Length 841
Best Local Similarity 33.1%; Pred. No. 3.4e-53;
Matches 219; Conservative 120; Mismatches 226; Indels
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Cibate: 10-May-2001 #Sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cibate: 10-May-2001 #Sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cibate: 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A,Reference number: A75000; MUID: 99069613; PMID: 9851916
A,Retes ewebsites genome. Wustl. edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C ele
A,Rote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A,Ratus: preliminary
A,Molecule type: DNA
A,Residues: 1-918 <STO>
A,Rotesidues: 1-918 <STO>
A,Cross-references: UNIPROT: P30645; GB:chr_III; PIDN: CAA78052.1; PID: g3878939; GSPDB:GNC
C;Genetics:
A,Genetics:
A,Rote of the Article of th
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Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase
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                           855 QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEBYEVPDLDGARAPING 914
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                                                                                                                                                                                                                                                                                                                                                                                Species: Caenorhabditis elegans
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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19.6%; Score 938.5; DB 2;
Best Local Similarity 30.3%; Pred. No. 3.6e-53;
Matches 243; Conservative 135; Mismatches 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 GOLSDNEEWSLQAVEK-HTLVALKRVQA------
                                                                                                                                                                                                                                                                                                                                                        protein R08D7.6 [imported] - Caenorhabditis elegans
                                                                                                                                               CCSLD 919
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CCSLE 927
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NiAlternate names: PDESAI
C;Species: Homo sapiens (man)
C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C;Accession: JW0106
R;Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S.C.
Biochem. Biophys. Res. Commun. 247, 249-254, 1998
A;Title: Molecular cloning and expression of human cGMP-binding cGMP-specific phosphodie
A;Reference number: JW0106; MUID:98308101; PMID:9642111
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A;Residues: 1-875 <STA>
K;Crose-references: UNIPROT:076074; GB:AJ004865; NID:g3355605; PIDN:CAA06170.1; PID:g335
C;Genetics:
A;Gene: GDB:PDE5A
                                                                                                                                                     ---SEDMOQLQSMLGCEVQAMLCVPVISRATDQVVALACAFWKLGGDLFTDQDEHVIQHC 349
                                                                                                                                                                                                                                                                                                           158 PHFSSFADELTDY----KTKNMLATPIMN--GKDVVAVIMAVNKLNGPFFTSEDEDVFLKY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 CERYSVGLLDMTK-EKEFFDVWSVLMGESQPYSGPRTPDGREIVFYKVIDYILHGKEBIK 328
PPD---CDSLRDLCQVEESTALLELVQDMQESINMERVVFKVLRRLCTLLQADRCSLFMY
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3,5'-cyclic-GMP phosphodissterase (EC 3.1.4.35) beta chain - human
C;becies Homo sapitans (man)
C;becies Homo sapitans (man)
C;becies Homo sapitans (man)
C;becies in A42228, 34350; 518715
R;Cocession: A42228, 34350; 518715
R;Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
R;Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
A; McEarence number: A42228; MUID:92347868; PMID:1322354
A; McEacher number: A42228; MUID:92347868; PMID:1322354
A; McEacher number: A42228; MUID:92347868; PMID:132354
A; McEacher number: Detailminary
A; McEacher number: Detailminary
A; McEacher number: A572; Disparage (MID:92347868; PMID:132354
A; McEacher number: Disparage (MID:92347868; PMID:132354
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A; McEacher number: A572; Disparage (MID:92347868; PMID:132354
A; McCassion: A4328
A; McCassion: S3450; MUID:93351644; PMID:839443
A; McCassion: S3450; MUID:93351644; PMID:335644; Muid:A572;                                                                                                                                                                                                                                                                                                                   168
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                                                                              359 GENHFHRASMMFFEDLGFSMLYKLNKRKLSYLVLRVSAGYRPVPYHWSHAFAVTHFCWL
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17.1%; Score 819.5; DB 2; Length 854;
Best Local Similarity 27.5%; Pred. No. 1.9e-45;
Matches 229; Conservative 157; Mismatches 327; Indels 119;
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A;Cross-references: GDB:9032947
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosp.
C;Keywords: alternative splicing; GMP binding; phosphorotein; phosphoric diester i
F;612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F;102/Binding site: phosphate (Ser) (covalent) by cGMP-dependent kinase) #status p
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RESULT A36617

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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine
N'Alternate names: CGMP phosphodiesterase beta chain
C;Species 10s primigenius taurus (cattle)
C;Species 28-Mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36617; 819145; S14011; S00251
C;Accession: A36617; 819145; S14011; S00251
C;Accession: A36617; Muradov, N.V.; Muradov, K.G.; Gui
J. Biol. Chem. 265, 12955-12959; 1990
A;Title: Beta-subunit of bovine rod photoreceptor CGMP phosphodiesterase. Comparison win
A;Reference number: A36617; MUID:90330632; PMID:2165490
A;Accession: A36617
A;Molecule type: mRNA
A;Residues: 1-853 -LIP
A;Cross-references: UNIPROT:P23439; GB:J05553; NID:gl62824; PIDN:AAA30440.1; PID:gl6282
A;Experimental source: retina
A;Experimental source: retina
A;Note: 40-Arg was also found
B;Lipkin, V.
B;Duhitted to the EMBL Data Library, December 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S00251
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 534-536, RRSWC', 542-596, 'Y', 598-601,'W', 603-606,'QLI' <0VC>
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide (C;Keywords: acetylated amino end; blocked amino end; cGMP; cGMP binding; phosphoric die P;2-853/Product: 3',5'-cyclic-GMP phosphodiesterase beta chain #status predicted <MAT>
F;556-789/Pomain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
P;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
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A;Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the algasterance number: S00161; MUID:88030033; PMID:2822478
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A,Accession: S19145
A,Accession: S19145
A,Accession: S19145
A,Rocession: S19145
A,Rocession: S19145
A,Rocession: S19145
A,Rocession: L-853 - L13 - A,Rocession: L-853 - L13 - A,Rocession: L-853 - L13 - A,Rocession: L-853 - L13 - A,Rocession: L-853 - L13 - 
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-2, P', 4-90, P', 92-93, 'H', 95-202, 'VN', 205-489, 491-853
A; Cross-references: EMBL:X57146
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16.7%; Score 799.5; DB 2; Length 853;
Best Local Similarity 26.2%; Pred. No. 3.9e-44;
Matches 221; Conservative 168; Mismatches 334; Indels 119
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Qy 342 DEHVIQHCFHYTSTVLTSTLAFQKEQKIKCECQALLQVAKNLFTHLDDVSVLLQEI 397	OY 398 ITEARNISNAEICSVFLLDQNELVAKVFDGGVVEDESY	Qy 436BIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFR 478	CGISIAHSLLYKKVN ::: : LGWSVLNTDTYDKMN	Qy 539 BAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDS 578 :: : :	Qy 579 -NFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHN 637	Qy 638 WMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAA 697	Qy 698 LYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIF 757	Qy 758 KDLQKNAREVGYDRINKQHHSLLLCLIAMISCDLSDQTKGWKTTRKIA 803 :::::	804 ELIYKEFPSQGDLEK-AMGNRPMEMMDREKA-YIPELQISFMEHIAMPIYKLLQDLFPKA	Db 739 LMVANEFWEÓGÖLÄRTVLQQQPIPMMÜRNKGDELPKLÖVGFIDFVCTFVYKEPSRFHKEI 798	Qy 862 AELYERVASNREHW 875 :::::: Db 799 TPMFDGLQNNRVEW 812	RESULT 9 A47451 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog C;Species: Canis lupus familiaris (dog) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A47451; S34290	Risuber, M.L.; Pittler, S.J.; Qin, N.; Wiight, G.C.; Holcombe, V.; Lee, K.H.; Crait, C.M. Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993 A;Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation A;Reference number: A47451; MUID:93248211; PMID:8387203 A;Accession: A47451	A;Status: preliminary A;Nolecule type: manA A;Residues: 1-85 _{A;Residues: 1-85 _{A;Residues: 1-1-10-10-10-10-10-10-10-10-10-10-10-10-}}	A, Note: sequence inconsistent with the nucleotide translation A, Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBIP:130783) R; Clements, P.J.	A;Reference number: \$34290 A;Accession: \$34290 A;Status: preliminary	A;Molecule type: mRNA A;Residues: 1-184,'D',186-856 <cle> A;Cross-references: EMB1:223014; NID:g312327; PIDN:CAA80557.1; PID:g312328 C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p C;Keywords: cGMP binding; phosphoric diester hydrolase</cle>
Qy 474 STGFRTRNILCPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLL 533	534 YKKVNEAQYKSHLANEMMYHMKVSDDEYTKLIHDGIQ	572 PVAALDSNFASFTYTPRSLPEDDTSMAILQDANFINNYKIDCPTLARFCLMVKKGYR 5.72 PVAALDSNFASFTYTPRSLPEDDTSMAILQDANFINNYKIDCPTLARFCLMVKKGYR 5.72 PVAALDSNFASFTYTPRSLPEDDTSMAILQDANFINNYKIDCPTLARFCLMVKKGYR 5.72 PVAALDSNFASFTYTPRSLPEDDTSMAILGDANFINNYKIDCPTLARFCLMVKKGYR 5.72 PVAALDSNFASFTYTPRSLPEDDTSMAILGDANFINNYKIDTSMAILGDANFASFTYNTHAFTYN TOTT TOTT TOTT TOTT TOTT TOTT TOTT T	DD 495 GPAKFDIYEFHFSDLECIELELVKCGIQMIYELGVVKRFQIPQEVLVKFLFSVSKGIK 552 QY 632 DPPYHNWMHAFSVSHFCYLLYKNLELINYLEDMEIFALFISCMCHDLDHRGTNNSFQVAS 691	Qy 692 KSVLAALYSSEGSVMERHFRAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLA 751	752 HHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTR ::::: : 673 I.YEKKRPMROJKTUDESKNYEDRKSWYEYLSLETTRKRIVMAMMMTACDLSATTKFWEVDG	801 KIAELIYKEFFSQDLEK-AMGNRPMEMMDREK-AYIPELQISFMEHIAMPIYKLLQDLF	859 PKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCC	DD 791 BEILFMFDKLQNNKKBWRALADEXEARVKALEBDQKKETTAKKVGIBICNGGFAFKSSIC 850 Qy 917 SL 918	Db 851 RI 852	RESULT 8	3'5'-cyclic-GWP phosphodiesterase (EC 3.1.4.35) - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004	150186 150186 3. L.; Green, D.A. 3. S9, 365-372, 1994 ecular characterization of the alpha'-subunit of cone photoreceptor cGMP phonumber: 150186; MUID:95121406; PMID:7821382 150186 ecilminary; translated from GB/EMBL/DDBJ	A, Residues: 1-862 <sem> A, Cross-references: UNIPROT:P52731, GB:L29233, NID:g495742, PIDN:AAC42223.1, PID:g495743 C, Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p C, Keywords: CGMP binding; phosphoric diester hydrolase F,561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <cmp></cmp></sem>	24;	Qy 194 GDQKGGVAYTNQDRKILQLCGELYDLDASSLQLKVLQYLQOETQASRCCLL 244	Qy 245 LVSBDNLQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDK 283 :	OY 284 KSIQLKDLTSEDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQ 341

A;Reference number: \$30762
A;Accession: \$30762
A;Accession: \$30762
A;Accession: \$30762
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A;Coss-references: UNIPROT:P23440; EMBL:X60133; NID:g53595; PIDN:CAA42719.1; PID:g53596
B;Bachr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FRIBS Lett. 278, 107-114, 1991

Library, June 1991

EMBL Data r: S30762

to the

A,Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha cing of the beta-subunit gene. A,Reference number: S13030; MUID:91130581; PMID:1847109

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                              Length
                             Query Match
16.7%; Score 799; DB 1; L.
Best Local Similarity 26.5%; Pred. No. 4.2e-44;
Matches 223; Conservative 161; Mismatches 331;
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A,Rolleule type: mRNA
A,Residues: 1-559,'d',561-856 <BA2>
A,Cross-references: EMBL:X60133
R,Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.
R,Bowes, C.; Li, T.; Danciger, M.)
R,Reference number: $13121; MUID:91015387; PMID:1977087
A,Reference number: $13121; MUID:91015387; PMID:1977087
A,Residues: 1-2, X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231,'R', 233-235
A,Residues: 1-2, X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231,'R', 233-235
A,Residues: 1-2, X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231,'R', 233-235
A,Rosserreferences: EMBL:X55968; NID:953616; PIDN:CAA9393-1; PID:953617
A,Rosserreferences: EMBL:X55968; NID:953616; PIDN:CAA9393-1; PID:953617
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\$30762
3'.5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse C;Species: Mus musculus (house mouse)
C;Becies: Alov-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Accession: \$30762; \$13031; \$13121

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A; Regidues: 1-855 <LIT>
A; Regidues: 1-855 <LIT>
A; Cross-references: UNIPROT: P16586; GB:M37838; NID:g163490; PIDN:AAA30687.1; PID:g163491
A; Cross-references: UNIPROT: P16586; GB:M37838; NID:g163490; PIDN:AAA30687.1; PID:g163491
B; Charbonneau, H.; Prusti, R.K.; LeTrong, H.; Sonnenburg, W.K.; Mullaney, P.J.; Walsh, K Proc. Natl. Acad. Sci. U.S.A. 87, 288-292
A; Title: Identification of a noncatalytic cGMP-binding domain conserved in both the cGMP A; Reference number: A34809
A; Accession: A34809
A; Accession: A34809
A; Accession: A34809
A; Accession: A34809
A; Residues: 308-502 <CHA>
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A;Note: parts of this sequence were confirmed by protein sequencing
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C;Reywords: c3MP binding; phosphoric diester hydrolase
F;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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C; Species: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C; Accession: A34810; A7, 293-297, 1990
A; Title: Bovine cone photoreceptor cGMP phosphodiesterase structure deduced from a cDNA A; Reference number: A34810; MUID:90115860; PMID:2153291
A; Status: preliminary
GVAQAINKKSGNGGTFTEKDEKDFAAYLAFCGIVLHNAQLYETSLLENKRNQVLLDLASL 329
                                                  LFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQ--NELVAKVFDGGVVEDESYEIRIP 440
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                                                                                545 HLANEMMYHMKVSDDEYTKL--LHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSM
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                                                                                                                                                                                     678 MFQKIVDESKNYEDKKSWVEYLSLETTRKEIVMAMMMTACDLSAITKPWEVQSKVALLVA
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28.3%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                       KLLH-------DGIQPVAAIDSNPAS-----FTYTPRSLP--EDDTSMAILSM 602
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                                                                                                                                                AGHVATTGOILNIPDAYA - - HPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNK
                                                                        | | : : | | :: | | | | | | | | | | LEVLLE-BAGSVELDVTPTSKF
                           EWSLQAVEKHTLVALKRVQALQQRESSV-APEATQNPPEEAAGDQKGGVAYTNQDRKILQ
                                                                                                                                    EVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLT---STLA
                                                                                                                                                                                                                                                          EISQETVEKYLEANPOPAKEYPNRKLQVEVPSGGAQAPASASPP---GRTLABEAALYLE
                                                                                                EDNLQLSCKVIGDKVLEREISPPLTTGRLGQVVEDKKSIQLKDL--TSEDMQQLQSMLGC
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Pred. No. 3e-43;
; Mismatches 331;
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A;Cross-references: UNIPROT:P51160; EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g11 A,Note: intron positions were determined by partial sequencing of genomic DNA (SY)catan A.S.; Piriev, N.I.; Parber, D.B. Gene 166, 205-211, 1995
A;Title: Isolation and characterization of a cDNA encoding the alpha' subunit of human A,Reference number: JC4520; MUID:96125191; PMID:8543163
A,Accession: JC4520
A,Molecule type: mRNA A,Residues: I-115,'V',117-269,'S',271-372,'P',374-463,'L',465-564,'Q',566-858 <VIC>A,Residues: I-115,'V',117-269,'S',271-372,'P',374-463,'L',465-564,'Q',566-858 CVIC>A,Rossidues: I-115,'V',117-269,'S',271-372,'P',374-463,'L',465-564,'Q',D',566-858 CVIC>A,Rossidues: I-115,'V',117-269,'S',271-372,'P',271-372,'P',271-372,'P',271-372,'P',271-372,'P',271-372,'P',271-372,
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F; 855/Psinding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTEEEAIKYVTVDPTKKE---IIMAMMTACDLSAITKPWEVQSQVALMVANEFWEQGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.9%; Score 758.5; DB 2; Length (
Best Local Similarity 25.8%; Pred. No. 1.9e-41;
Matches 208; Conservative 151; Mismatches 299; Indels
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A; Molecule type: protein
A;Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3
A;Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;215-282;297-306;312-330;361-3
A;Moleci this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S:
R;Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.;
R;Ovchinnikov, Y.A.; Gupanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.;
A;Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A;Reference number: S00161; MUID:88030033; PMID:2822478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-193, 'V', 195-423, 'T', 425-674,'F', 676-859 <PIT>
A; Residues: 1-193, 'V', 195-423, 'T', 425-674,'F', 676-859 <PIT>
A; Cross-references: GB:MZ6043; NID:g162833; PIDN:AAA30443.1; PID:g162834
C; Comment: This protein is involved in the transduction and amplification of the visual
C; Superfamily: 3', 5'-cyclic-GMP phosphodiesterase alpha chain; 3', 5'-cyclic-nucleotide po
C; Keywords: acetylated amino end; CGMP; heterotrimer; phosphoric diester hydrolase; reth:
F; 2-859/Product: 3', 5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <AM?
F; 558-791/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F; 2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ripittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen, Genomics 6, 272-283, 1990
A; Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodia, A; Reference number: A34611; MUID:90169986; PMID:2155175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-859 <0V1>
A;Cose-references: UNIPROT:P11541; EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617
A;Accession: 827007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.,5.-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine N.Alternate names: cGMP phosphodiesterase alpha chain c;Species: Bos primigenius taurus (cattle) c;Species: Bos primigenius taurus (cattle) c;Species: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: S06418; S27007; S00161; A34611; S08516 T.M.; Bystrov, N.A.; Gubanov, VV.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.T.M.; Bystrov, N.S.; Severtsova, I.V.; Lipkin, V.M. Dokl. Biochem. 296, 303-307, 1987 A;Tile: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the A;Reference number: S06418
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                                                                                                                                                                                                                                                                                     759 DLOKMAE-----VGYDRTNKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIY 807
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                                                                                                                                                                                                                       620 HGS--SILERHHLEFGKFLLAEESLNIYQNLNRRQHEHVIHLMDIAIIATDLALYFKKRT
                             MHAPSVSHPCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAAL
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A;Residues: 1-859 <0V2>
A;Residues: 1-859 <0V2>
A;Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A;Cross-references: Bequence was confirmed by protein sequencing
A;Note: 381.Val was also found
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                                                                                                                                                                                                                                                                                                                                                                                                                   808 KEFFSQGDLEK-AMGNRPMEMMDREK-AYIPELQISFMEHIAMPIYKLLQDLF 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||: |||||: : :|: |||| | :|:||: ||: :|| | | AEFWEOGDLERTVLDOOPIPPMDRNKAAELPKLOVGFIDFVCTFVYKFPLGIF 790
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Best Local Similarity 25.8%; Pred. No. 3.5e-41;
Matches 218; Conservative 148; Mismatches 335;
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                                                                                                                                                                                                                                          RESULT 14
$13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
R;Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A;Reference number: 61030; MUD:91130581; PMID:1847109
A;Reference number: 813030; MUD:91130581; PMID:1847109
A;Residues: 1-800 cBAB>
A;Cross-references: UNIPROT:062037; EMBL:X60133
R;Baehr, W.
Submitted to the EMBL Data Library, June 1991
A;Reference number: 830762
A;Molecule type: DNA
A;Residues: 1-559, "R',561-800 cBA2>
A;Molecule type: DNA
A;Residues: 1-559, "R',561-800 cBA2>
A;Molecule type: DNA
A;Residues: 1-559, "R',561-800 cBA2>
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphoric diester hydrolase
C;Keywords: alternative splicing; CGMP binding; phosphoric diester hydrolase
F;556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cGMP phosphodiesterase alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQLKDLT----SEDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDEDVFTKYLNFATLNLK---IYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHKA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 FYTVRAYLNCERYSVGLLDMTK-EKEFFDVWPVLMGBAQPYSGPRTPDGREIVFYKVIDY 319
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906.5 18	906.5	901	106	899	897	845.5	841.5	821.5	805.5	804.5	804	801.5	799

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of human cDNAs encoding a cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase.";

Gene 19:189-95(1997).
-!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)0 = nucleoside 5'-phosphate.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain, and Hippocampus;
MEDLINE-97354299; PubMed-9210593; DOI=10.1016/S0378-1119(97)00046-2;
Rosman G.J., Martins T.J., Sonnenburg W.K., Beavo J.A., Ferguson K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=000408-3; Sequence=Not described; IsSSUE SPECIFICITY: Expressed in brain and to a lesser extent in heart, placenta, lung, skeletal muscle, kidney and pancreas sIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).
                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=3;
Comment=Additional isoforms seem to exist. Experimental
confirmation may be lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=000408-2; Sequence=Not described;
941 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=000408-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: Contains 1 GAF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM PDE2A3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67733; AAC51320.1; -. Genew; HGNC:8777; PDE2A.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PDE2A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PDE2A3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PDE2A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loughney K.;
HUMAN
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PDE2A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GLGFSDLPGKPLARLVAPLAPDTQVLVMPLADKEAGAVAAVILVHCGQLSDNEEWSLQAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EKHTLVALRRVQVLQQRGPREAPRAVQNPPEGTAEDQKGGAAYTDRDRKILQLCGELYDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 VEDKKSIQLKDLISEDVQQLQSMLGCELQAMLCVPVISRATDQVVALACAFNKLEGDLFT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DODEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 LQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA 840
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                     TAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNWM
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPPCADSLQDALLSLGSVIDV
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                   GO; GO:0004118; F:cGMP-stimulated cyclic-nucleotide phosphodi.
                                                                                                                                                                                                                                                                                                                                     96.3%; Score 4728.5; DB 1; Length 941; 96.0%; Pred. No. 2e-273; tive 18; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                          633 891 Catalytic (By similarity).
941 AA; 105716 MW; 9797609B487FD64E CRC64;
                                  InterPro; IPR003018; GAP.
InterPro; IPR003018; GAP.
InterPro; IPR003073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase I; 1.
PRINTS; PR000397; PDIESTERASE1.
SWART; SW00065; GAF; 2.
FROSTER; PS00126; PDEASE I; 1.
Alternative splicing; GGMP; Hydrolase; Membrane.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.0 Matches 904; Conservative
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RC STEADLE FROM N. N. S. Water A. M. Schuler S. J. Scholer S. M. Strubberg R. L., Feingold E. N., Grouse L. H., Derge J. G., Struberg R. L., Feingold E. N., Grouse L. H., Derge J. G., Struberg R. L., Feingold E. N., Ghemmen C. M., Schuler G. D., Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K., Altschul S. F., Jordan H., Moore T., Max S. I., Wang J., Haibe F., Boatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L. M. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T. L., Scheetz T. E., Rapleton M., Goares M.B., Donaldo M.F., Casavant T. L., Scheetz T. E., Brownstein M. J., Uddin T. B., Toshiyuki S., Carninci P., Frange C., Raha S. S., Loquellano N.A., Peters G. J., Abramson R. D., Mullahy S. J., Raha S. S., Loquellano N.A., Peters G. J., Abramson R. D., Hulyk S. W., Rilalon D.K., Muzny D. M., Sodergren E. J., Lu X., Glibs R. A., Rahay J., Helton E., Ketteman M., Rodarigues S., Sanchez A., Matring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ratinger A.C., Grimwood J., Scheuutz J., Myers R.M., Butterfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S. J., Marra M.A.;
Rodriguez A.C., Marra M.A.;
Rad Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitteed (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC040974; AAH40974.1;
GO; GO:000414; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.

GO; GO:0003124; F:catalytic activity; IEA.

GO; GO:0007165; F:signal transduction; IEA.

InterPro; IPR003048; GAF.

InterPro; IPR003009; Met_phos_hydro.

InterPro; IPR002073; PDEase.
                                                                                                                      841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Pfam; PF01203; PDEase I; 1.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM0047; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
SROOTIS; PS00126; PDEASE I; 1.
SROUNCE 941 AA; 105648 MW; 93028FC28CB54D6B CRC64;
                                                                                                                                                                                                                                                                             901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE 942
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U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphodiesterase 2A, cGMP-stimulated.
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(CGSPDE)

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stimulated phosphodiesterase) (CGS-PDE)
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MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPQPCADSLQDALLSLGSVIDV
               MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPQQCADSLQDALLSLGSVIDI
                                                                                                     GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
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CN2A_BOVIN STANDARD; PRT; 921 AA.
P14099; Q28664;
01-3An-1990 (Rel. 13, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stimulated cyclic nucleotide
                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM PDE2A1).
MEDLINE-91373395; PubMed=1654333;
Sonnenburg W.K., Mullaney P.J., Bevo J.A.;
"Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase cDNA. Identification and distribution of isozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINES 7092242; PubMed=3025833;
MEDLINES 7092242; PubMed=3025833;
Mearbonneau H., Beier N., Walsh K.A., Beavo J.A.;
Identification of a conserved domain among cyclic nucleotide phosphodiesteraes from diverse species.";
Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312(1986).
-!-FUNCTION: Hydrolyzes both cyclic AMP (CAMP) and cyclic GMP (CGI-IC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O nucleoside 5'-phosphate.
-!-SUBCELLULAR LOCATION: Membrane-bound (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=P14099-2; Sequence=VSP 004555; SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Heart;
MEDLINE-91104948; PubMed-2176866;
le Trong H., Beier N., Sonnenburg W.K., Stroop S.D., Walsh
                                                                                                                                                                                                                                                                                                                    Juilfs D.M., Sonnenburg W.K., Seraji S., Beavo J.A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
Name=PDE2A1;
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Name=PDE2A2;
IsoId=P14099-3; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Beavo J.A., Charbonneau H.;
"Anaino acid sequence of the cyclic GMP
phosphodisterase from bovine heart.";
Biochemistry 29:10280-10288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 GAF domain.
                                                                                                                                                                                                                                                Biol. Chem. 266:17655-17661(1991)
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InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase I; 1.
SMRNTS; PR00387; PDIESTERASE1.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM PDE2A3)
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 592-921 FROM N.A.
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                                   taurus (Bovine).
                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PDE2A3;
                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart;
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EMBL; U21101; AAA63683.1; -.
EMBL; W94540; AAA6922.1; -.
PIR; UC2486; JC2486.
RGD; 620965; Pde2a.
                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                 STANDARD;
                                                   GCCSLDAE 942
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GCCSLDAE 921
                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PDE2A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PDE2A3
                                                                                                                                                                                 Name=Pde2a;
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Q01062;
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                                GAF.
Catalytic.
N-acetylmethionine.
MRRQPAASRDLEAPERGQOVFLKPDEPPPPQPCADS (in isoform PDE2A3)
/FIId=VSP_004555.
N -> D (in Ref. 2).
P -> L (in Ref. 4).
MW; E29F4C9975E83640 CRC64;
                                                                                                                                                                                                            EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKE 154
                                                                                                                                                                                                                                                                                                                       SCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV 334
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                cGMP; Direct protein sequencing
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                                                                                                                                     Length 921;
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                                                                                                                                    Score 4657; DB 1;
Pred. No. 3.6e-269;
3; Mismatches 7;
     PROSITE; PS00126; PDEASE 1; 1.
Acetylation; Alternative splicing; cG
Hydrolae; Membrane.
DOMAIN 352 530 GAF.
DOMAIN 613 871 Catalyti
MOD RES 1 1 N-acetyl
VARSPLIC 1 25 MRSQPASE
                                                                                                                 921 AA; 103227 MW;
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98.9%;
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633
SM00471; HDc; 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                              913
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                                                                                          (cGMP)
                                                          LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPIN
794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE=95110334; PubMed=7811274;
Yang Q., Pankind M., Bolger G., Thompson W.J., Repaske D.R.,
Cutler L.S., Epstein P.M.;
"A novel cyclic GMP stimulated phosphodiesterase from rat brain.";
Biochem. Biophys. Res. Commun. 205:1850-1858(1994).
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TISSUE SPECIFICITY: Brain.
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CGMP-dependent 3',5'-cyclic phosphodiseterase (EC 3.1.4.17)
GMP stimulated phosphodiseterase) (CGS-PDE) (CGSPDE).
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                                                                                                                       279 Catalytic (By similarity). 546 W -> R (in Ref. 2). 558 L -> M (in Ref. 2). 104663 MW; EPOBSCIE266EAB18 CRC64;
InterPro; IPR003018; GAP.
InterPro; IPR003007; Met_phos_hydro.
InterPro; IPR003007; Met_phos_hydro.
InterPro; IPR002073; PDEase.
Pfam; PP01590; GAR; 2.
Pfam; PP01590; PDEase I; 1.
PRINTS; PR00387; PDIESTERASE1.
SWART; SW00471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
Alternative splicing; CGMP; Hydrolase; Membrane.
                                                                                                                                                                                                    33;
                                                                                                                                                                              90.0%; Score 4418; DB 1; 92.4%; Pred. No. 6.6e-255;
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758 7
928 AA;
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Best Local Similarity
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CONFLICT
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**X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Reblike=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., N. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska M.A.; Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Sundaratha J., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Sundaratha J., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Sundaratha J., Sundaratha J., Marra M.A., Schein J.E., Jones E.D., Sundaratha J., Marra M.A., Schein J
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                                                                                                                                                                              EHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVP
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PubMed=12271124; DOI=10.1073/pnas.192374899;
Martinez S.B., Wu A.Y., Glavas N.A., Tang X.-B., Turley S.,
Hol W.G.J., Beavo J.A.;
"The two GAP domains in phosphodiesterase 2A have distinct roles in dimerization and in cGMP binding.";
Proc. Natl. Acad. Sci. U.S.A. 99:13260-13265(2002).
-! FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (CGMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-PEB-2003 (Rel. 41, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
GMP stimulated phosphodiesterase) (CGS-PDE) (GGSPDE).
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-i- SUBUNIT: Homedimer.
-i- SUBCELLULAR LOCATION: Membrane-bound (Potential).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Q92254; Q8K2U1;
28-FEB-2003 (Rel.
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Pfam; PF00233; PDEase
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Indels
                                                                                                                                                                                                                                                                                                                                                                        348 526 GAP.
609 867 Catalytic (By similarity).
421 422 GMP binding.
407 407 GMP.
916 AA; 103287 MW; 51C03B086633BF20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 88.9%; Score 4366.5; DB 1, Similarity 90.5%; Pred. No. 7.6e-252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Mismatches
                                                                                                                                                                                 EMBL, BC006845, AAH06845.1; -.
EMBL, BC029810, AAH29810.1; -.
EMBL, BC057029; -; NOT ANNOTATED CDS.
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                                                                                                            854 AYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 RGOQVFLKPDEPPPPPPPCADSLQDALLSLGSVIDVAGLQQAVKBALSAVLPKVETVYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 685 AA; 78177 MW; A6087394B98221C3 CRC64;
                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16750.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.1%; Score 3345; DB 2; Best Local Similarity 71.5%; Pred. No. 4.5e-191; Matches 656; Conservative 9; Mismatches 3;
                                                                                                                                                                                                                                                                                     685 AA
                                                                                                                                                                          LDFLDEEYEVPDLDGARAPINGCCSLD 940
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                                                                                                                                                                                          LDFLDERYEVPDLDGTRAPVNGCCSLE
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0387; PDIESTERASEL.
SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
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95 -EEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDK 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AGDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQOETQASRCCLLLVSEDNLQ
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                                                                                                                                                                                                                                                                                                  Query Match 33.8%; Score 1659.5; DB 2; Length Best Local Similarity 40.3%; Pred. No. 2.2e-90; Matches 351; Conservative 160; Mismatches 265; Indels
                                                                                                                                                                                                                                                          F4CA1EE8B23A9E0E CRC64;
GO, GO:0003824; F:catalytic activity; IEA.
GO; GO:000165; P:signal transduction; IEA.
InterPro; IPR003018; GAP.
InterPro; IPR003018; GAP.
InterPro; IPR002073; PDEBSE.
Pfam; PF01590; GAF; 2.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00047; PDIESTERASE1.
SMART; SM00411; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 819 AA; 92145 MW; F4CALEE8B23A9E
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                                                                                                                                                                      325 GCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAF
                                                                                                                                                                                                                                                            128 QKEQKIKCECQALLQVAKOLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                               248 CFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 SHLANEMMYYMKVSDDEYTKLLHDGIQPVAAIDSNPASFTYTPRSLPEDDTSMAILSML
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                                                    265 LLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSML
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MEDLINE=99015760; PubMed=9801141; DOI=10.1016/S0014-5793(98)01150-8;
KOyanagi M., Suga H., Hoshlyama D., Ono K., Iwabe N., Kuma K.,
Miyata T.;
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096076;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 26, Last annotation update)
BFPDE2.
Ephydatia fluviatilises. Demospongiae; Ceractinomorpha; Haplosclerida; Spongillidae; Ephydatia.
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117 HLVYAEFFAEGDLEKQMGLRPNAMMDRKKACIPMLQIEFLTTVIRPTFEILVQIFPETGS
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PFfam; PF00233; PDEase I; 1.
PRINTS; PR003387; PDIESEI.
SMART; SM00065; GAF; 2.
SMART; SM0471; HDC; 1.
PROSTIE; PS00126; PDEASE I; 1.
SEQUENCE 1544 AA; 171689 MW; F5254E0CCDB3D065 CRC64;
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Larity 32.0%; Pred. No. 3.7e-50;
Conservative 150; Mismatches 306; Indels
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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477 FLDTIDSNREQWERV
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Best Local Similarity
Matches 246; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 TTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 QPVAAIDS---NFASFTYTPRSLPEDDTSMAI-LSMLQDMNFINNYKIDCPTLARFCLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                 Anopheles gambiae etr. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBL_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; AAABO1008964; EAA12229.1; --
GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. ..
InterPro; IPR003018; GAF.
InterPro; IPR003018; GAF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 1236; DB 2; Length 491; 50.5%; Pred. No. 1.9e-65; ive 91; Mismatches 138; Indels 16
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                                                                                                                                                                                                                           (TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Ebip6713 (Fragment)
Name=ebiG6713; ORFNames=ENSANGG0000005075;
                                                                                                                                                             Z
                       491
HIAMPIYKLLQDLFPKAAELYERVASNREHW
                                                                                                                                                                                                        Created)
                                                                                                                                                           PRT;
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Pfam; PF00233; PDEase I; 1.
PRINTS; PR00397; PDIESTERASE1.
PROSITE; PS00126; PDEASE I; 1.
                                                                                                                                                                                                     (TrEMBLrel. 26,
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Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SD13096p.
Name=Pdell; Synonyms=CG10231;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Artropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
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Genew, HGNC1873; ENGIA...; COLNED.
Genew, HGNC1873; PDE11A...
GO, GO:0004112; F:cyclic-nucleotide ph
InterPro; IPR003018; GAF.
InterPro; IPR003007; Met_phos hydro.
InterPro; IPR002073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00331; PDEase I; 1.
PRINTS; PR00387; PDIEĞTERASE1.
SMART; SM00471; HDC; 1.
AB048417; BAB62712.1; JOINED.
AB048418; BAB62712.1; JOINED.
AB048419; BAB62712.1; JOINED.
AB048420; BAB62712.1; JOINED.
AB048421; BAB62712.1; JOINED.
AB048421; BAB62712.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.7%; Pre
Matches 249; Conservative 160;
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                                                                                                                                                                                             #WAEEPRALLRAMSMTVCDLSAITKPWEIEKRVADLVSSEFFEGGDMEKQELNITPIDIM 1143
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                                           735 AIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILLATDLAHHLRIFKD----LQKMAEVGYD 790
                                                                                                                                                                                                                                                                                                                                                                                                     DREKA-YIPELQISFMEHJAMPIYKLLQDLFPKAAELYERVASNREHW-----TKVS 900
                                                                                            DTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWMHAFSVSHFCYLLYK
                                                                                                                  675 NLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQ
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20469516; PubMed=10906126; DOI=10.1074/jbc.M003041200;
Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
"Isolation and characterization of two novel phosphodiesterase PDE11A
variants showing unique structure and tissue-specific expression.";
J. Biol. Chem. 275:31469-31479(2000).
                     YKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPED
                                                                                                                                                                                                                                                                                                                           RTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGN-RPMEMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=20570133; PubMed=11121118;

Wands K., Kanoh Y., Okumura K., Omori K.;

Yuasa K., Kanoh Y., Okumura K., Omori K.;

"Genomic organization of the human phosphodiesterase PDE11A gene:

Bvolutionary relatedness with other PDEs containing GAF domains.";

EMBL, ABOS6704; BAB16371.1;

EMBL; ABO36704; BAB16371.1;

EMBL; ABO48423; BAB62712.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ODOEPEEEQOQONVISNGDCKAMSDDDVAASEAEVAVDSPSEKASVNG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HKFTIRGLPSNNSL-----DFLDEEYEVP-DLDGARAPING 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, E
Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphodiesterase 11A (Phosphodiesterase 11A4).
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BAB62712.1; JOINED.
BAB62712.1; JOINED.
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAB62712.1;
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BAB62712.1;
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AB048404;
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AB048414;
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AB048416;
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.c-nucleotide phosphodiesterase activity; NAS.
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                                                                                                                                                                                                                                                                                                                                                         Score 986; DB 2; Length 934;
Pred. No. 4.1e-50;
); Mismatches 321; Indels 8
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SEQUENCE 934 AA; 104810 MM; 994675824259447E CRC64;
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                                                                                       NNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRD
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                                                                   EDM--QQLQSMLGCEVQAMLCVPVISRATD-QVVALACAFNKL-GGDLFTDQDEHVIQHC
                                                                                                                                        FHYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEI
                                                                                                                                                                                                                                            CSVLLLEDIESPVVKP----TKSPELMSPKCSADAENSFKESMEKSSYSDWLINNSIA
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AYOS8470; AAL13699.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Brydroidea; Drosophilidae; Drosophila.
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Last annotation update)
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LKPMLDSVATNRSKWEELHQKRLLASTASSSS
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Name=Pde6; Synonyms=CG8279;
271 NLQLSCKVIGDKVLE-
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831 AELVTSEFFEGGDRERLELKLTPSAIFDRNRKDELPRLOLEWIDSICMPLYQALVKVNVK
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20570113; PubMed=11121118;
Yuasa K., Kanoh Y., Okumurra K., Omori K.;
"Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
Eur. J. Blochem. 268:168-178(2001).
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 988 AA; 111169 MW; 7F678869353DF7EB CRC64;
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Last annotation update)
                                                      LKPMLDSVATNRSKWEELHQKRLLASTASSSS 922
                                882 AAELYERVASNREHWTKVSHKFTIRGLPSNNS 913
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AB048402; BAB62713.1;
AB048403; BAB62713.1;
AB048404; BAB62713.1;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                            Phosphodiesterase 11A3.
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AB048409;
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AB048418;
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EMBL; AB
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                                                                                                                                                                                                173 EEWSLQAVEKHTLVALKRVQA-LQQRESSVAPEATQNPPEE--AAG---DQKGGVAYTDQ 226
                                                                                                                                                                                                                   EKW---LTERAPPEALSRLOEFIENRKPHKRPSVTSDLFOOWMAASPTVOOKSPRSLSNS 114
                                                                                                                                                                                                                                                     SASSLPECRRILMDLDEGELFMELIRDVANELDIDVLCHKILVNVGLLTHADRGSLFLAK 174
                                                                                                                                                                                                                                                                                 268 -SEDNLQLSCKV-----IGDKVLE---EEISPPLTTGRLGQVVEDKKSIQLKDLTSE 315
                                                                                                                                                                                                                                                                                                                          DMQQLQSMLGCEV-----QAMLCVPVISRATDQVVALACAFNKLGGDL-FTDQDEHV 366
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           .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679 TNYLEDMEIPALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNTHGCNI FDH FSRKDYQRMLDLMRDI ILATDLAHHLRI FKDLQKMAEVG-YDRTNKQHH
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                                                                                                                                                                              Gaps
                                                                                                                                                      Query Match 20.1%; Score 986; DB 2; Length 1018;
Best Local Similarity 30.3%; Pred. No. 4.6e-50;
Matches 263; Conservative 151; Mismatches 327; Indels 126;
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       GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase GO; GO:0003824; F:catalytic activity; IEA.
GO:0007165; P:signal transduction; IEA.
                                                                                                                       PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;
                                      InterPro; IPR003018; GAF.
InterPro; IPR003007; Met_phos_hydro.
InterPro; IPR003073; PDEase.
Pfam; PF01590; GAF; 2.
Pfam; PF00233; PDEase_I; 1.
PRINTS; PR00387; PDIESTERASE1.
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SMART; SM00471; HDC; 1
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REMINEACIONE S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Randon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballaw R.M., Bauw A., An H.J., Andrews-Frankoch C., Baldwin D.,

RA Besson K.Y., Bence P.V., Barman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller C., Davemport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Burtis K.C., Busam D.A., Buller C., Perraz C., Ferraz C., Perrica C., Ferraz C.,

RA Burtis K.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Well W.H., Ibegwam C.,

Adalah M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum K.A.,

RA Harris N.L., Matter S., McIntosh T.C., Morris J., Woshrefi A.,

Randro P., Lei, Y., Leviteky A.A., Li J., Li Z., Linn X.,

Rallah M., Ralush F., Karpen G.H., Ke Z., Kennison J.A.,

Randro P., Lei, Y., Leviteky A.A., Li J., Li Z., Linn X.,

Randro P., Lei Y., Leviteky A.A., Li J., Mixon K., Woshrefi A.,

Rollon D.R., Woly M., Wixon K., Wosher D.N., Woelred J.,

Rollon D.R., Woly M., Wixon K., Wosher S., Wosher S., Wosher S.,

Randres R., Pecter C., Throre R., Wenter B., Wall H.,

Spier R., Sparding A.C., Standers R.D., Scheeler F., Shen H.,

Randres R., Wolders E.W., Rubin G.W., Weissenbach J.,

Randres R., Wolders E.W., Rubin G.W., Venter J.C.,

Randres R., Wollin G.W., Wolley K.C., Wu D., Yang S., Yao Q.A., Yelliams S.M., WoodageT,
    876
818 LPKMQVGFIDVICLPLYRVLCDTFPWITPLYEGTLENRRNWQDLABKVEM-GLTWIDHDT
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; meinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Pde6; ORFNames-CG8279;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            1131 AA
                                                                                 LDFLDEEY-----EVPDLDGARAPIN
                                                                                                                                   Created)
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
A. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Sandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A. Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
B. Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
B. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dewis B.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A. Durbin K.J. Evangelista C.C., Ferriera S., Fleischmann W.,
R. Fosler C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K.,
A. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                  856 IPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLP--SNNS 913
                                                                                                               STQAILCMPIMNAQKKVIGVAQLINKANGVPFTDSDASIFEAFAIFCGLGIHNTQMYENA
                                                                                                                                                                                                                                          461 KCERCSVFLVDLDCCEASHLEKIIEKPNQPATRAIKSADSFEEKKMRNRFTVLFELGGEY
                                FDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFR-----
                                                                                            -TRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKV
                                                                                                                                                            559 NEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSM
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bodoterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=Pde11; ORFNames=CG10231;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRKILQLC------GELY-----DLDASSLQLKVLQYLQQETQASRCCLLLV- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 -SEDNLQLSCKV-----IGDKVLE---EEISFPLTTGRLGQVVEDKKSIQLKDLTSE 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 DMQQLQSMLGCEV-----QAMLCVPVISRATDQVVALACAFNKLGGDL-FTDQDEHV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., IEA.
                                                          Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-2245069; Pubmed=12537572;
MINISTRE-2245069; Pubmed=12537572;
MINISTRE-2245069; Pubmed=12537572;
MINISTRE-2245069; MINISTRE G.H., Prochnik S.E.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drygdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome: a
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Pred. No. 5.4e-50;
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                              a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002)
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                                               MEDLINE=22426070; PubMed=12537573;
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30.3%;
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

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Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,

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                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22436065; PubMed=12537568; MEDLINE-22436065; PubMed=12537568; MEDLINE-22436065; PubMed=12537568; MEDLINE-22436065; PubMed=12537568; Medliker S.E., Wheeler D.A., Kronmiller B., Farise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Parls B. V., Pfeiffer B.D., Richards S., Sodergren B.J., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426070; PubMed=12537573;
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Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Hang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: systematic review.";
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Submitted (MAR-2004) to the
EMBL; AE003659; AAF53675.2;
FlyBase; FBgn0032686; Pdell.
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Pfam; PF00233; PDEase_I; 1.
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                                                                                                      Length 1365;
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PR0SITE; P00126; PDEASE I; 1.
SEQUENCE 1365 AA; 151173 MW; B0562EFDF5012E56 CRC64;
                                                                                                                       Local Similarity 31.2%; Pred. No. 1.1e-49; nes 247; Conservative 150; Mismatches 307;
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                                                                                                        20.0%; Score 983; DB 2; 31.2%; Pred. No. 1.1e-49;
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1063 VDSPSEKASVNG 1074
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164 VHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAP-----EATQNPPE-- 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 HYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEIC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21393948; PubMed=11502204;
MEDLINE=21393948; PubMed=11502204;
Yuana K., Ohgaru T., Asahina M., Omori K.;
Viantification of rat of rat and human PDE11A; comparison of rat and human PDE11A splicing variants.";
Eur. J. Blochem. 268:4440-4448(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                Eur. J. Biochem. 268:4440-4448 (2001).

EMBL. ABGS9562; BAR795629.1; -

GO; GO:0004114; F:31',5'-cyclic-nucleotide phosphodiesterase GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0007145; F:signal transduction; IEA.

Fiam; PPO1590; GPF: 2.

Pfam; PF001590; GPF: 2.

Pfam; PF00233; PDEase I; 1.

SMART; SM00065; GAF: 2.

SMART; SM00471; HDc: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 247; Conservative 158; Mismatches 312; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 935 AA; 104570 MW; E80F1039770F8276 CRC64;
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%; Score 974; DB 2; 30.8%; Pred. No. 2.1e-49;
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                Phosphodiesterase 11A4.
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                                                                                                      NCBI_TaxID=10116;
                                   Name=RNPDE11A4;
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Search completed: June 26, 2005, 12:21:50 Job time : 136.465 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 26, 2005, 12:09:51; Search time 32.3607 Seconds (without alignments) 2800.810 Million cell updates/sec

4911 1 MGQACGHSILCRSQQYPAAR......VPDLDGARAPINGCCSLDAE 942 US-10-697-894-43 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: seq length: 0 seq length: 200000000 Minimum DB Maximum DB

283416

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Sc	Score	% Query Match	* Query Match Length	DB	SUMMAKIES	Description
4	657	94.8	921	-	A40981	3',5'-cyclic-nucle
4	41	90.0	928	Н	JC2486	3',5'-cyclic-nucle
_	938	σ	841	٦	S24462	'n
4	938	19.1	918	~	D88544	protein R08D7.6 [i
5 821	1.5	16.7	854	7	A42828	ΜP
804	4.5	16.4	862	~	150186	
_	804	16.4	875	Н	JW0106	'-cyclic-GMP
8 801	1.5	16.3	853	~	A36617	
	801	16.3	856	Н	A47451	•
	794	16.2	875	-	A48719	'-cyclic-GMP
	791	16.1	856	~	830762	'-cyclic-GMP
	788	16.0	855	~	A34810	
	8.5	15.4	828	~	JC4520	
	756	15.4	800	~	S13032	
	3.5	15.3	859	Н	S06418	
	9.5	15.1	859	N	813030	
	726		859	~	B34611	-GMP
	969	14.2	393	N	T25590	cal prot
	1.5	8.2	859	N	AC2089	2
	390.5	8.0	664	N	T24459	hypothetical prote
_	3.5	7.8	712	7	871626	b
	2.5	7.8	673	~	I61358	3',5'-cyclic-nucle
	1.5	7.8	549	~	T16769	hypothetical prote
	0.5	7.7	584	~	B53109	3',5'-cyclic-nucle
	0.5	7.7	672	~	161259	3',5'-cyclic-nucle
	0.5	7.7	988	~	A54442	3',5'-cyclic-nucle
	9.5	7.7	536	7	I67945	3',5'-cyclic-nucle
80	7	7.7	562	~	159143	CAMP phosphodieste
	7	7.7	564	N	A40949	cyclic-AMP phospho

3',5'-cyclic-nucle	phosphodiescerase 3',5'-cyclic-nucle	phosphodiesterase	3',5'-cyclic-nucle	hypothetical prote	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-nucle	adenylate cyclase	cAMP phosphodieste	3',5'-cyclic-AMP p	3',5'-cyclic-nucle
167946	J53865 JC1519	I61354	S65543	T14783	A44162	A46378	A44161	A45334	T10796	JC6129	AB2044	B33904	A47286	S55348
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7.6	9.7	7.6	7.4	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.7	6.7	6.7	9.9
375	374	374	363.5	350	345.5	343.5	341.5	341	340	335.5	330.5	329	327	325.5
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 A40981
	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
_	NyAlternate names: cGMP-dependent phosphodiesterase
_	C;Species: Bos primigenius taurus (cattle)
	C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text change 09-Jul-2004
	C; Accession: A40981; B36112; A36112; B26650; A60179; C26650
	R;Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.
	J. Biol. Chem. 266, 17655-17661, 1991
	A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiester
	A; Reference number: A40981; MUID: 91373395; PMID: 1654333
-	A;Accession: A40981
	A; Molecule type: mRNA
	A;Residues: 1-921 <son></son>
	A;Cross-references: UNIPROT:P14099; GB:M73512; NID:g162829; PIDN:AAA74559.1; PID:g1628
	R;Le Trong, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; C
	Biochemistry 29, 10280-10288, 1990
	A, Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodie
	A; Reference number: A36112; MUID:91104948; PMID:2176866
	A;Accession: B36112
	A;Status: not compared with conceptual translation
_	A; Molecule type: mRNA
	A;Residues: 592-921 <let></let>
	A;Accession: A36112

ras

A; Molecule type: protein

A;Residues: 1-203, 10', 205-477,'0', 479-921 <LET2>
R;Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.
R;Charbonneau, H.; Beier, N.; Walsh, R.A.; Beavo, J.A.
A;Reference number: A26650, MUID:87092242; PMID:3025833
A;Reference number: A26650, MUID:87092242; PMID:3025833
A;Residues: 613-632,'L',634-794;808-868 <CHA>
A;Residues: 613-632,'L',634-794;808-868 <CH

A; Molecule type: mRNA A; Residues: 311-803, DV', 806-921 <TAN> A; Note: part of this sequence was confirmed by protein sequencing C; Comment: This protein is not glycosylated. C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, CGMP-stimulated; 3',5'-cyclic-C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase to TeMP binding; CGMP F; 655-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD> F; 1/Modified site: acetylated amino end (Met) #status experimental

ö Gapa ö Query Match 94.8%; Score 4657; DB 1; Length 921; Best Local Similarity 98.9%; Pred. No. 3.4e-293; Matches 898; Conservative 3; Mismatches 7; Indels

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          CEPVPPGSGDGALQDALLSLGSVIDVAGLQQAVKEALSAVLPKVETVYTLLDGESRLVC
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                                            AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPEATQNPPEEAA
                                                                                GDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCLLLVSEDNLQL
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                                                                                                                                             SCKVIGDKVLEBEISPPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCV
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RESULT 2

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated N;Alternate names: cGMP-dependent phosphodiesterase (S.Species: Rattus norvegicus (Norway rat) C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-20 C;Accession: JC2486 JC2486

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NIPDHFSRKDYQRMLDLMRDIILATDLAHHLRIPKDLQKMAEVGYDRTNKQHHSLLLCLL

09-Jul-2004

R;Yang, Q.; Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstei Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994
A;Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.
A;Reference number: JC2486; MUID:95110334; PMID:7811274
A;Accession: JC2486
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-928 c/XaN>
A;Residues: 1-928 c/XaN>
A;Residues: 1-928 c/XaN>
A;Experimental source: brain
B;Superfamily: 3, 5'-cyclic-nucleotide phosphodiesterase, CGMP-stimulated; 3',5'-cyclic-C;Reywords: alternative splicing; cAMP binding; homodimer; phosphoprotein; F;643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology cCNPD>
F;109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted SHLANEMMYHMKVSDDEYTKLIHDGIQPVAAIDSNFANFTYTPRSLPEDDTSMAILSML VLVIPLLDKETGTVAAVILVHCGQLSDSEEQSLQVVEKHALVALQRVQALQQRR ---PE VFDGGVVDDESYEIRIPADQGIAGHVATTGQILMIPDAYAHPLFYRGVDDSTGFRTRNIL RGQQVFLKPDEPPPPPQPCADSLQDALLSLGSVIDVAGLQQAVKRALSAVLPKVETVYTY LLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCNGLGPSDLPGKPLARLVAPLAPDTQ VLVI PLVDKEAGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQQRESSVAPE ATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDLDASSLQLKVLQYLQQETQASRCCL LLVSEDNLQLSCKVIGDKVLBEBISFPLTTGRLGQVVBDKKSIQLKDLTSEDMQQLQSML VFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNIL CPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYR SHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSML Gaps . 9 Query Match 90.0%; Score 4418; DB 1; Length 928; Best Local Similarity 92.4%; Pred. No. 1e-277; Matches 846; Conservative 31; Mismatches 33; Indels 셤 8 6 6 6 6 8 & 8 8 6 6 6 ð

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protein ROBD7.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spacesion: D88544
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biologation elegance number: A75000; MUID: 99065613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elcaps.phiote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D88544
A;Accession: D88544
A;Accession: D88544
A;Residues: 1-918 <STO>
A;Residues: 1-918 <STO>
A;Construction: Caenore Caen
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C;Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase
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                                                                                                                  DRINKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMM
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1.6e-52;
thes 226;
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19.1%; Score 938; DB
Best Local Similarity 33.1%; Pred. No. 1.6e-
Matches 219; Conservative 120; Mismatches
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                                                                                                                                                                                                                                                                                                      probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) R08D7.6 - Caenorhabditi probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) R08D7.6 - Caenorhabditis by probable 1',5'-cyclic-nucleotide protein R08D7.6 - C;5pecies: Caenorhabditis elegans C;5pecies: Caenorial S41041; S24462 T. R;Ainscough, R.; Hawkins, T. R;Ainscough, R.; Hawkins, T. Ribars DNA A;Reference number: S41036 A;Accession: S41041 AIN A;Residues: 1-481 AAIN A;Residues: 1-481 AAIN A;Residues: UNIPROT:P30645; EMBL:Z12017 A;Residues: T.;Ainscough, R.; Waterston, R.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; Grawkins, T.; Ainscough, R.; Waterston, R. Wature 356, 37-41, 1992 A;Ttle: The C. elegans genome sequencing project: a beginning. A;Reference number: S24457; MUID:92168156; PMID:1538779 A;Contents: annotation C;Genetics: A;Interns: 31/1; 97/3; 179/2; 260/1; 296/3; 324/3; 622/2; 701/3; 775/3 C;Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase homology cCNPD> F;403-627/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology cCNPD>
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                                                          DSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSL
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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 150186
R;Semple-Rowland, S.L.; Green, D.A.
Exp. Eye Res. 59, 365-372, 1994
A;Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP pho A;Reference number: 150186; MUID:95121406; PMID:7821382
A;Reference number: T50186
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1.862 <SEM>
A;Cross-references: UNIPROT:P52731; GB:L29233; NID:g495742; PIDN:AAC42223.1; PID:g495743
A;Cross-references: UNIPROT:P52731; GB:L29233; NID:g495742; PIDN:AAC42223.1; PID:g495743
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide pickeywords: cGMP binding; phosphoric diester hydrolase
F;561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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389 VNKKEEIVGVATFYNRKDGKPFDEQDEVLMESLTQFLGWSVMYTDTYDKMYKLENRKDIA
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                                                                                                           371 FHYTSTVLTSTLAFQKEQKLKCEC---QALLQVAKNLFTHLDDVSVLLQEIITEARNLSN
                                                                                                                                                                          LNFATLYLK---IYHLSYLHNCETRRGOVLLWSANKVFEELTDIEROFHKAFYTVRAYLN
                                                                                                                                                                                                                                                                                                                                                                                              460 I----PAD-----QGIAGHVATTGQILNIPDAYAHPL--FYRGVDDSTGFRTRNILCFPI
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larity 27.7%; Pred. No. 6.4e-44;
Conservative 137; Mismatches 302; Indels 135
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Matches 220;
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A42828
3,5'-CYClic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Mar. 1933 #sequence
C;Date: 04-Mar. 1935
R;Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
C;Date: 04-Mar. 1933 #sequence
C;Date: 04-Mar. 1933
R;Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
Genomics 13, 688-704, 1923
A;Ritle: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re
A;Reference number: A42828; MUID:92347868; PMID:1322354
B;Rhramtsov, N.V.; Peahchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki
FEBS Lett. 327, 275-278, 1933
A;Rocession: 334590; MUID:93351644; PMID:839443
A;Ritle: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu
A;Reference number: 334590; MUID:93351644; PMID:839443
A;Residues: D*Sate 1881. 1864 A*R.
A;Residues: D*R.
A;R
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A;Map position: 4p16.3-4p16.3
C;Superfamily: 3',5'-cyclic-dMp phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide C;Superfamily: 3',5'-cyclic-nucleotide C;Keywords: cGMP binding; phosphoric diester hydrolase F;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                  849
                                                                                                                                                                                                                                                                                                                           DREKAYIPELQISFMEHIAMPIYKLLQDLFPKAABLYERVASNREHWTKVSHKFTIRGLP 909
                                                                                                                                                                                                                                                                                                                                                             209 PPEEAAGDOKGGVAYTDODRKILOLCGELYD-LDASSLQLKVLOYLQOETQASRCCLLLV 267
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                                                                          DRINKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMM
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A;Cross-references: EMBL:X62694
C;Genetics:
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larity 27.5%; Pred. No. 5e-45;
Conservative 158; Mismatches 3
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A36617
3',5'-cyclic-GMP phosphodiesterase (BC 3.1.4.35) beta chain - bovine
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JW0106
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human
N;Alternate names: PDE5A1
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JW0106
R;Stacey, P: Rulten, S:; Dapling, A.; Phillips, S.C.
Biochem. Blochem. Brophys. Res. Commun. 249-254, 1998
A;Title: Molecular cloning and expression of human cGMP-binding cGMP-specific phosp
A;Reference number: JW0106; MUID:98308101; PMID:9642111
A;Accession: JW0106
A;Molecule type: mRNA
A;Residues: 1-875 <STA>
A;Cross-references: UNIPROT:O76074; GB:AJ004865; NID:g3355605; PIDN:CAA06170.1; PII
C;Genetics:
A;Gene: GDB:PDE5A
A;Cross-references: GDB:9032947
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                                                                        KSIQLKDLTSED--MQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQ 362
                                                                                                                                                                                                                                                                                                                                       : : | : | | | | | | | : | : | : | KLENKKDIAQEMLMYQTKATPTEVESILKYKEKLAVKSIEECDEKDLIRILKBELPDPKD 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDLQKMAE------VGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELIYKEFFSQGDLEK-AMGNRPMEMMDREKA-YIPELQISFMEHIAMPIYKLLQDLFPKA 882
9
                                           100 icrsrngipevatriinvtptskfednl-----Vnpdk----Ervppldiglagwyahtk
                                                                                          151 KPRNIPDVKKNNHPSDYLDKKTGYTTVNMMAIPITQ--GKEVLAVVMALNKLNASEFSKE
                                                                                                                                                                                                                                      324 ILHGKEEIKVIPTPPADHWCLISGLPTYVAENGFICNMANAPADBYFTFQKGPVDETGWV
GDVKEGVSFKDMSR--LEECN1LFELLTE1QDEAGSMEK1VHKTLQRLSQLLARDRCSMF
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                                                                                                                       DEHVIQHCFHYTSTVL----TSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEI
                                                                                                                                                                                                                        -----BIRI----PAD-----QGIAGHVATTGQILNIPDAYA--HPLFYRGVDDSTGFR
                                                                                                                                                                                                                                                                        500 TRNILCPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVN
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C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodi C;Superfamily: 9',5'-cyclic-nucleotide phosphodiesterative splicing; GMP binding; phosphodiesterase homology cCNPD>
F;612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology cCNPD>
F;102/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predi
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                                                                                                                                           Gaps
                                                                                                                                           Indels 124;
                                                                                                   DB 1; Length 875;
                                                                                                   16.4%; Score 804; DB 1; Lilarity 28.7%; Pred. No. 7e-44; Conservative 154; Mismatches 322;
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Best Local Similarity
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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog C;Species: Canis lupus familiaris (dog) C;Species: Canis lupus familiaris (dog) C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A47451; S3420 R;Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M F;Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M Froc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993 A;Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation A;Reference number: A47451; MUID:93248211; PMID:8387203
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C;Superfamily: 3',5'-cyclic-chep phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide
C;Reywords: CGMP binding; phosphoric diester hydrolase
F;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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                                               495 GPAKFD--IYEFHFSDLECTELELVKCGIQMYYELGVVRKFQIPQEVLVRFLFSVSKGYR
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A;Experimental Source: Irish setter, retina
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBIP:130783)
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larity 26.5%; Pred. No. 1.1e-43;
Conservative 162; Mismatches 330; Indels 128;
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A; Accession: $34290
A; Status: preliminary
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submitted to the EMBL Data
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A;Residues: 1-856 <SUB>
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N.Alternate names: cGWP phosphodiesterase beta chain
C;Species Bob primigantius taurus (catta)
C;Species In Salariagentius taurus (catta)
R;Lipkin, V.M.; Kiramicov, N.V.; Vaslievskaya, I.A.; Atabekova, N.V.; Muradov, K.G.; Gub
R;Lipkin, V.M.; Kiramicov, N.V.; Vaslievskaya, I.A.; Atabekova, N.V.; Muradov, K.G.; Lose-1, 2563, 12955-12959, 1990
A;Title: Beta-aubunit of bovine rod photoreceptor CGNP phosphodiseterase. Comparison wit
A;Rocession: A36617
A;Rocession: A36617
A;Rocession: Edge-in Will
A;Rocession: Edge-in Will
A;Rocession: Babi. Data Library, December 1990
A;Rocession: Siglas
A;Rocess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 QETQASRCCLLLVSEDN--LQLSCKVIG---DKVLEE-----EISFPLTTGRLGQVVE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQEIITEARNLSNAEICSVFLLDQNE-------
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A;Cross-references: GB:L16545
A;Experimental source: lung
X:Thomasa, M.K.; Prancis, S.H.; Corbin, J.D.
J. Biol. Chem. 265, 14971-14978, 1990
A;Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding A;Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding A;Reference number: A35807; MUD:90368672; PMID:2168396
A;Reference number: A35807
A;Reference potential and a cGMP-binding A;Residues: 90-101 cTMO>
A;Residues: 90-101 cTMO>
A;Residues: 90-101 cTMO>
C;Superfamily: J;S'-cyclic-GMP phosphodiesterase 5A; 3',S'-cyclic-nucleotide phosphodisterase homology cCNPD>
F;602-825/Domain: 3',S'-cyclic-nucleotide phosphodiesterase homology cCNPD>
F;92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predic-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 HLDVTALCHKIFLHIHGLISADRYSLFLVCEDSSNDKFLISRLFDVAEGSTLEBASNNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALACAFNKLGGD - - LFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQALLQVAKN
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11 Similarity 28.4%; Pred. No. 3.1e-43;
240; Conservative 154; Mismatches 334; Indels 116;
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Best Local S:
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A48719
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
N'Alternate names: PDE5A1
C;Species: Bos primigenius taurus (cattle)
C;Species: Dos primigenius taurus (cattle)
C;Daccession: A48719, A35807
R;McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecek, A.; Seger, D.; Le Trong, H.; Coll A;Reference number: A48719; MUD:94043054; PMID:8226796
A;Reference number: A48719; MUD:94043054; PMID:8226796
A;Reference number: A68719
A;Residues: 1-875 <MCA>
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   88
                                                     307 IQLKDLTS--EDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDE
                                                                                                                 HVIQHCFHYTSTVLTSTLAFQKEQKLKCEC---QALLQVAKNLFTHLDDVSVLLQEIITE
                                                                                                                                                                                                                                                    264 VRAYLNCDRYSVGLLDMTK-EKEFFDVWPVLMGBAQPYSGPRTPDGREIVFYKVIDYILH
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   PEHVAGACGDGQPTDCASFRELCQVEBSAALFELVQDMQESVNMERVVFKILRRLCTILR
                                 ASRCCLLLVSEDN--LQLSCKVIG---DKVLEE-----EISFPLTTGRLGQVVEDKKS
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rodesule type: mRNA
A;Rossiues: 1-855 <LIT>
A;Cross-references: UNIPROT:P16586; GB:M37838; NID:g163490; PIDN:AAA30687.1; PID:g163491
R;Charbonneau, H.; Prusti, R.K.; LeTrong, H.; Sonnenburg, W.K.; Mullaney, P.J.; Walsh, K
Proc. Natl. Acad. Sci. U. S.A. 87, 288-292, 1990
A;Title: Identification of a noncatalytic cGMP-binding domain conserved in both the cGMP
A;Reference number: A34809; MUID:90115859; PMID:2153290
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A,Residues: 308-502 ccHA>

A,Residues: 308-502 ccHA>

A,Cross-references: GB:M33140; NID:g163492; PIDN:AAA30688.1; PID:g163493; GB:M29465

A,Note: parts of this sequence were confirmed by protein sequencing

A,Note: parts of this sequence were confirmed by protein sequencing

C,Superfamily: 3',5'-cyclic-GMP phosphoric diester hydrolase

C;Reywords: CGMP binding; phosphoric diester hydrolase

P;556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology cCNP>
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C;Accession: A34810; A34810; A34810; M.L.
R;Li, T.; Volpp, K.; Applebury, M.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 293-297, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 293-297, 1990
A;Title: Bovine cone photoreceptor cGMP phosphodiesterase structure deduced from a cDNA A;Reference number: A34810; MUID:99115860; PMID:2153291
A;Accession: A34810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Bos primigenius taurus (cattle)
C.Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                             560 RHGFNVAQTMFTLLMTGKLKSYYTDLEAPAMVTAGLCHDIDHRGTNNLYQMKSQNPLAKT
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                                                                       440 KLENRKDIAQDMVLYHVRCDKDEIQBILPTRDRLGKEPADCEEDELGKILKEELPGPTKP
                                                                                                            ---SFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNW
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                          JC4520

3'.5' -cyclic-GMP phosphodiesterase (BC 3.1.4.35) alpha' chain - human

C'Species: Homo sapiens (man)

C'Species: Homo S63688 JC4520

R'Feshchenko, B.A.; Andreeva, S.G.; Suslova, V.A.; Smirnova, B.V.; Zagranichny, V.E.;

FBBS Lett. 381, 149-152, 1996

A,Title: Human cone-specific cGMP phosphodiesterase alpha' subunit: complete cDNA seq

A,Reference number: S63688 MID:9619393; PMID:8641425

A,Residues: 1-958 «FES.

A,Residues: 1-958 «FES.

A,Residues: 1-958 «FES.

A,Residues: 1-958 «FES.

A,Cross references: UNIRROT:P51160; EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g

A,Residues: Introm positions were determined by partial sequencing of genomic DNA

R;Viczian, A.S.; Piriev, N.I.; Farber, D.B.

Gene 166, 205-211, 1995

A,Title: Isolation and characterization of a cDNA encoding the alpha' subunit of huma

A,Recession: JC4520

A;Molecule type: mRNA
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A;Residues: 1-115,'V',117-269,'S',271-372,'P',374-463,'L',465-564,'Q',566-858 <VIC>A;Cross-references: GB:U31973; NID:g940230; PIDN:AAA96392.1; PID:g940231
A;Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional residencie:
C;Genetics:
A;Gene: alpha'.pde
A;Introns: 160/3, 21/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/3;
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide [C;Keywords: CGMP binding; lipoprotein; phosphodiesterase hydrolase; photoreceptor; pre: F;560-770.Domain: 24.5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F;561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F;855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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ERTVIQQQPIPMMDRNKRDELPKLQVGFIDFVCTFVYKEPSRFHKEITPMLSGLQNNRVE 811
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                                                                                                                                                                                                                                                                                                                                                                                  SRLLDVTPTSKFEDNL-----VGP---DKEVVFPLDIGIVGWAAHTKKTHNVPDVKKNS
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                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      Indels 147;
                                                                                                                                                                                                                   15.4%; Score 758.5; DB 2; Length 858;
25.8%; Pred. No. 6e-41;
                                                                                                                                                                                                                                                    Conservative 151; Mismatches 299;
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372 HYTSTVLTSTLAFQKEQKLKCEC---QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNA 428
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                                                                                                                                                                                                                                                                                                               ,5'-cyclic-GMP phosphodiesterase
                                   780 DLQKMAE-
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A, Molecule type: mRNA
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RESULT 14
$13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse .
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
R;Baehr, W.; Champagne, M.S; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A;Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha c; R;Reference number: S13032
A;Reference number: S13032
A;Reference number: S13032
A;Residues: 1-800 cARA
A;Residues: S10762
A;Molecule type: DNA
A;Residues: S10762
A;Molecule type: DNA
A;Residues: 1-559,'R',561-800 cBA2>
A;Residues: 1-559,'R',561-800 cBA2>
A;Residues: 1-559,'R',561-800 cBA2>
A;Residues: 1-559,'R',561-800 cBA2>
A;Cross-references: BNA
A;Residues: 1-559,'R',561-800 cBA2>
C;Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase homology cCNP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 ITEARNLSNAEICSVFLLDONELVAKVFDGGVV---EDESY
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NiAlternate names: cGMP phosphodiesterase alpha chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S06418; S27007; S00161; A46611; S08516
R;Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zar
T.M.; Bystrov, N.S.; Severtsova, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987
A;Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3
A; Residues: 2-11;22-27;32-40;95-98;112-105;180-193;248-267;275-282;297-306;312-330;361-3
A; Residues: 2-27;3-712;734-736;751-760;766-771;787-798;911-819 <-000.
A; Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S; R; Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.B.; R; Ovchinnikov, Y.A.; 199-173, 1987
A; Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha, A; Reference number: S00161; MUID: 88030033; PMID: 2822478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: S00161
A,Accession: S00161
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fesidues: 1-659 <0V2>
A,Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A,Note: part of this sequence was confirmed by protein sequencing
A,Note: 381-Val was also found
B;Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
A,Fitler, Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
A,Reference number: A34611; MUID:90169986; PMID:2155175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-193,'V',195-423,'T',425-674,'P',676-859 <PIT>
A;Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834
C;Comment: This protein is involved in the transduction and amplification of the visual C;Comment: This protein is involved in the transduction and amplification of the visual C;Superfamily: 3',5'-cyclic-GMP phosphodiestrase alpha chain; 3',5'-cyclic-nucleotide p. C;Keywords: acetylated amino end; CGMP; heterotrimer; phosphoric diester hydrolase; reti F;2-859/Product: 3',5'-cyclic-mached effects are alpha chain #status experimental <MA F;28-9791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CMP>
F;2-Modified site: acetylated amino end (Gly) (in mature form) #status experimental
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A;Molecule type: mRNA
A;Ressidues: 1-859 <0V1>
A;Ressidues: 1-859 <0V1>
A;Cross-references: UNIPROT:P11541; EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617
A;Accession: $27007
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		DRYSVGLLDMTK-QKEFFDVWPVLMGEAPPYAGPRTPDGREINFYKVIDYILHGKEDIKV 331	PADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCPPIK 509	IPNPPPDHWALVSGLPTYVAQNGLICNIMNAPSEDFFAFQKEPLDESGWMIKNVLSMPIV 391		NKKEEIVGVATFYNRKDGKFFDEMDETLMESLAQFLGWSVLNPDTYELMNKLENRKDIFQ 451	EMMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPR 609	DWVKYHVKCDNEBIQTILKTREVYGKEPWECEEBELABILQGELPDADKYEINKFHFSDL 511		PLTELELVKCGIQMYYELKVVDKFHIPQEALVRPMYSLSKGYRRITYHNWRHGFNVGQTM 571	YLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALYSSEGSVMER 729	FSLLVTGKLKRYFTDLEALAMVTAAFCHDIDHRGTNNLYQMKSQNPLAKLHGSSILER 629	HHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKDLQKWAB 786	HHLEFGKTLLRDESLNIFQNLNRRQHEHAIHMMDIAIIATDLALYCKKRTWFQKIVDQSK 689	VGYDRINKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIABLIYKBFFSQG 835	TYETQOEWTQYWMLDQTRKEIVMAMMMTACDLSAITKPWEVQSKVALLVAABFWEGG 746	DLEK-AMGNRPMEMMDREKA-YIPELQISFMEHIAMPIYKILQDLFPKAAELYERVASNR 893	DLERTVLQQNPIPMMDRNKADELPKLQVGFIDFVCTFVYKEFSRFHEEITPMLDGITNNR 806	EHWIKVSHKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCC 937	KEWKALADEYETKMKGLBEEKQKQQAANQAAAGSQHGGKQPGGGPASKSCC 857	
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Search completed: June 26, 2005, 12:23:00 Job time : 36.3607 secs

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OM protein - protein search, using sw model

June 26, 2005, 12:06:11; Search time 117.813 Seconds (without alignments) 3092.423 Million cell updates/sec Run on:

US-10-697-894-43 4911 Title: Perfect score:

1 MGQACGHSILCRSQQYPAAR......VPDLDGARAPINGCCSLDAE 942 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum 1 Maximum 1

seq length: 0 seq length: 200000000 88 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1906:*
2: geneseqp1900:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
7: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	Cyclic-GM	Cyclic GM	cGS-PDE a	Bovine br	Cyclic-GM		Bovine br	Bovine br	Bovine cG	CGS PDE f	Cyclic-GM	pHcgs6n c	Human cGS	Human cGS	Cyclic-GM	Human cyc	Human cGS	Human pho	Human pho	Human cGM	Human cGM	Human int	Human bra	Human src	Human Pro
	Description	Aar69728	Aaw11239	Aaw18049	Aaw71225	Aaw77041	Aaw60753	Aay80985	Abu58724	Adq94963	Aar28408	Aar69729	Aaw11253	Aaw18050	Aaw71226	Aaw77042	Aaw60754	Aay80986	Aae07954	Aae07918	Aab85117	Aab85106	Aag66539	Abu58725	Add14154	Ade62314
	ID	AAR69728	AAW11239	AAW18049	AAW71225	AAW77041	AAW60753	AAY80985	ABU58724	ADQ94963	AAR28408	AAR69729	AAW11253	AAW18050	AAW71226	AAW77042	AAW60754	AAY80986	AAE07954	AAE07918	AAB85117	AAB85106	AAG66539	ABU58725	ADD14154	ADE62314
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عد	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.5	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3
	Score	4911	4911	4911	4911	4911	4911	4911	4911	4911	4871	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5	4728.5
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ALIGNMENTS

Cyclic-GMP stimulated nucleotide phospho-diesterase, antibodies; bovine adrenal cortex; hormones; neurotransmitters; transmission regulation; enzyme purification; clone pBBCGSPDE-7. Cyclic-GMP stimulated nucleotide PDE clone pBBCGSPDE-7. AAR69728 standard; protein; 942 AA (revised)
(first entry) 25-MAR-2003 11-OCT-1995 AAR69728; RESULT 1 AAR69728

Bos taurus

US5389527-A.

14-FEB-1995.

92US-00872644. 20-APR-1992;

91US-00688356, 19-APR-1991;

(UNIW) UNIV WASHINGTON.

Beavo JA; Sonnenburg WK, Charbonneau H,

WPI; 1995-090205/12. N-PSDB; AAQ83977.

New nucleic acid encoding cyclic-GMP stimulated nucleotide phosphodi:esterase - and related vectors and transformed cells, useful for screening cpds. for phospho-di:esterase modulating activity.

Example 5; Col 79-86; 69pp; English.

ţ AAQ81977 encodes AAR69728 the bovine brain cyclic-GMP stimulated nuclectide phospho-diesterase (CaM PDE) clone pBBCGSPDB-7. Eukaryotic cells that express CaM PDE can be used to screen cpds. for the ability modulate caM PDE activity. CaM PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers. Antibodies raised against CaM PDE can be used for enzyme purificn., or determination. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 942 AA;

Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; adrenal gland; cGMP; transmembrane signal; extracellular hormone; neurotransmitter; antibody.

Cyclic GMP stimulated phosphodiesterase.

(first entry)

(revised)

25-MAR-2003 17-MAR-1997

AAW11239;

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                                                            MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPPQPCADSLQDALLSLGSVIDV
                                                                                                                    61 AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEBPPHELPQBGKVREAVISRKRLGCN
                                                                                                                                      AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN
                                                                                                                                                                               GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNBEWSLQAV
                                                                                                                                                                                                                                          EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
                                                                                                                                                                                                                                                                                                   DASSLOLKVLQYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQV
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 Length 942;
                               Indels
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Query Match
100.0%; Score 4911;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches
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encoding cGMP-stimulated phospho:di:esterase - for prodn.

Beavo JA;

Charbonneau H, Sonnenburg WK,

WPI; 1997-033573/03.

N-PSDB; AAT51090

DNA

(UNIW) UNIV WASHINGTON

91US-00688356. 94US-00297494

19-APR-1991; 20-APR-1992; 29-AUG-1994;

US5580771-A

taurus.

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03-DEC-1996

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This sequence represents the cyclic GMP stimulated phosphodiesterase (GGS -PDE) clone pBBCGSPDE-5 isolated from bovine brain. This sequence is nearly identical to the bovine adrenal gland GGS-PDE isozyme. The cyclic nucleotide phosphodiesterases (PDBS) catalyse the hydrolysis of 3', 5' cyclic nucleotide monophosphates. The PDEs are therefore important in the control of the cellular concentration of cyclic nucleotides. The PDEs are therefore important in the control of the cellulate of transmembrane signals or second messenger are, in turn, regulated by transmembrane signals or second messenger cole in regulating the flow of information from extracellular hormones, neurotransmitters, or other signals that use the cyclic nucleotides as messengers. PDEs are present in most of the cells and tissues of messengers. PDEs are present in most of the cells and tissues of cukaryotic organisms, but only in trace amounts cGS-PDE are stimulated by cGMP in effecting cAMP hydrolysis. This is thought to occur through a normalytic cGMP specific site present on the cGS-PDE. The DNA encoding this sequence can be used for the production of recombinant cGS-PDE, which may have therapeutic and diagnostic uses. This sequence may also be currect PP field.)
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AAW11239 standard; protein; 942 AA

RESULT 2 AAW11239 ID AAW11

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The present sequence represents the pBBCGSPDE-7 bovine brain insert amino acid sequence. The large open reading frame encodes a 942-readine polypeptide that is nearly identical to the adrenal gland cyclic-GMP-stimulated phosphodisererase (GGS-PDE) isozyme. The difference in the primary structure of the two isozymes lies in the amino-terminal residues remaining carboxy-terminal residues 1.5 of the adrenal GGS-PDE, and residues in both are identical. The DNA sequences of the GGS-PDE's are used for the production of the recombinant earymes, which in turn may be used for antibody production and to screen for compounds that modulate phosphodisererase activity. (Updated on 25-MAR-2003 to correct PI
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                                                                                                 Charbonneau H,
                            91US-00688356.
  94US-00297510
                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                            WPI; 1997-131799/12
                                                                                                                                            N-PSDB; AAT67223.
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  29-AUG-1994;
                             19-APR-1991;
                                            20-APR-1992;
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level. They are controlled by second messengers e.g. Ca2+ and calmodulin and transmembrane signals and through pathways involving these, regulate flow of information from extracellular hormones, neurotransmitters and other signals using cyclic mucleotides as messengers. The specification describes an assay for identifying a chemical agent which modifies the enzymatic activity of a mammalian CaM-PDE. The assays are useful for identifying modulators of CaM-PDEs. The assays is carried out by incubating cells expressing CaM-PDE with the suspected modulator and measuring its effect e.g. monitoring the hydrolysis of CAMP and/or CGMP
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                                                        EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
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bovine brain, is one of several phosphodiseterases isolated in this invention. The phosphodiseterases were used to transform host cells, preferably mammalian or yeast cells. The recombinant proteins and fragments produced can be used for therapeutic, diagnostic, and prognostic purposes and will provide the basis for preparation of monoclonal and polytolonal antibodies. An antibody specific for the ca2+/calmodulin-stimulated cyclic nucleotide phosphodiseterase (PDE) polypeptide is useful for affinity purification or detection of the polypeptide and is selective only for the Ca2+/calmodulin stimulated
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Calmodulin stimulated phosphodiesterase; therapeutic; antibody
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Assay for inhibitors of cyclic guanidine monophosphate-stimulated nucleotide phosphodiesterase, potentially useful as cardiotonic agents,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine brain cGS-PDE, SEQ ID NO:43.
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92US-00872644.
94US-00297494.
95US-00455525.
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N-PSDB; AAZ90380.
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29-AUG-1994;
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                                                                                                                                                                                                                                           phosphodiesterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV 180
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                                                                                                                                                                                                                                                                                                                 The present sequence represents cyclic-GMP-nucleotide phosphodiesterase (cGS-PDE), and is isolated from bovine. The specification describes calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterases (CaM-PDEs). CaM-PDEs are characterised by their responsiveness to intracellular calcium, which leads to a decreased intracellular concentration of cAMP and/or cGMP. CaM-PDEs, and their fragments or synthetic peptides, are used in and their reagencies and diagnosis. They are also used to generate specific antibodies useful as immunoassay reagents for detecting the protein or for affinity purification and for identifying specific modulators of CaM-PDE activity. CaM-PDEs are implicated in signalling involving extracellular hormones and neurotransmitters, so selective inhibitors are potentially useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiotonic, antidepressant, antihypertensive and antithrombotic agents
                                                                                                                                                                                                                                                      e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEBPPHELPQEGKVREAVISRKRLGCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPPPCADSLQDALLSLGSVIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKHTLVALKRVQALQORESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT
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                                                                                                                                                                                                                                       New calmodulin and calcium stimulated cyclic nucleotide phosphodies - used e.g to identify selective modulators, potentially useful as cardiotonic, antidepressant, antihypertensive agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 4911; 100.0%; Pred. No. 0;
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                                                                                                                                                                            Charbonneau H,
                                                                                                91US-00688356.
92US-00872644.
94US-00297494.
                                                                          95US-00479532
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                                                                                                                                                    WASHINGTON
                                                                                                                                                                                                    WPI; 1998-398038/34.
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                                                                                                                                                 UNIW ( WIND)
                                                                                                                           29-AUG-1994;
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                       US5776752-A
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SEGSVWERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOKMAEVGYDRTINKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGNR PMEMMDREKAYI PELQI SFMEHIAMPI YKLIQDL PPKAAELY ERVASNREHWTKVS
                                                                 DAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA
                                                                                                                                                                                                                                                                                                                                               HAFSVSHFCYLLYKNLELTNYLEDME1FALF1SCMCHDLDHRGTNNSFQVASKSVLAALY
                                                                                                                                                                                                                                                                                                                                                                               SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
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                                                                                                                                                             FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN
                                                                                                                                                                                                                                                      FASFTYTPRSLPEDDTSMAILSMLODMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
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The invention relates to purified and isolated polynucleotide sequence encoding a mammalian Ca^2+/calmodulin- or cyclic GMP-stimulated cyclic conclosed phosphodiesterase polypeptide (CaMP-DE and cGS-PDE). Also included are a DNA vector comprising the novel DNA sequence, a host cell transformed with the polynucleotide sequence, a polypeptide product of the expression in the transformed host cell, an antibody specifically immunoreactive with the polypeptide and assay methods for identifying a chemical agent which modifies the enzymatic activity of a mammalian CaMP-DE or cGS-PDE. Disclosed are the cDNA and protein sequences of bovine S9KDB CAM-PDE, 61kDB CAM-PDE, G3kDB CAM-PDE, cGS-PDE and human 61kDa CAM-
                                                                                                                         SSEGSVMERHHFAQAIAILMTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
                                                                                                                                                                                                                                           LOKMAEVGYDRITNKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
                                   661 HAFSVSHFCYLLYKNLELTNYLEDMBIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY
                                                                                                SSEGSVMERHHFAQA IAILNTHGCNI FDHFSRKDYQRMLDLMRDI ILATDLAHHLRI FKD
                                                                                                                                                                                                                                                                                            MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVS
     HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified and isolated DNA sequence encoding a mammalian calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide phosphodiesterase polypeptide, useful for therapeutic, diagnostic prognostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cow; Ca2+/calmodulin stimulated phosphodiesterase; enzyme; $250A caM-PDE; GGS-PDE; GSADE CAM-PDE; GGS-PDE; CyClic-GMP-stimulated phosphodiesterase; cardiotonic agent; antidepressant; anti-hypertensive; anti-thrombotic.
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92US-00872644.
95US-00455526.
98US-00123783.
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20-APR-1992;
31-MAY-1995;
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                                                                                   The invention relates to purified and isolated nucleotide sequences encoding mammalian Ca2+/calmodulin-stimulated phosphodiesterases (CaM-PORS) and cyclic guantidine monophosphate (CSM)-stimulated phosphodiesterases (CGS-PDES). In particular the invention relates to assay for identifying chemicals that modify the enzymatic activity of amammalian cGS-PDE. The PDES catalyse the hydrolysis of of cyclic nucleotides to their corresponding 5'-uncleoside monophosphates. In this way they control the callular concentration of cyclic nucleotides, thereby regulating the flow of information from extracellular hormones, thereby regulating the flow of information from extracellular hormones, control messengers. The PDEs in turn are regulated by transmembrane signals or second messenger ligands such as Ca2+ or cGMP. Inhibitors of these enzymes are potentially useful as cardiotonics, antidepressants, antidepressants, antidepressants, antidepressants, antidentify specific inhibitors of particular isoforms of CGS-PDES. CAMPROSSS 4AY80966, and CAM-PDES and CGS-PDES from bowlnes
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their ability to alter a heat-shock phenotype.
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Best Local Similarity 100.0%;
Matches 942; Conservative 0;
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PDE and cGS-PDE. The DNA sequence is useful for producing a polypeptide having the enzymatic activity of a mammalian CaM-PDE or cGS-PDE which is used in therapeutic, diagnostic and prognostic applications and in the preparation of antibodies. Isolated chemical agents which are inhibitors of PDEs may have anti-depressant, anti- hypertensive or anti-thrombotic activities or may be cardiotonic agents. The present sequence is a Bovine CaM-PDE or cGS-PDE (or fragment) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Ca 2+/ calmodulin stimulated cyclic nucleotide phosphodiesterase; cGMP; cyclic-guanosine monophosphate; cGS-PDE; cyclic-GMP stimulated cyclic nucleotide phosphodiesterase; bovine.
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ive 0; Mismatches
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BENTLEY J K.
CHARBONNEAU F
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N-PSDB; ADQ94962.
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20-APR-1992;
29-AUG-1994;
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28-JUL-1998;
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A bovine brain cDNA library in lambda ZAP was screened with a 450 bp BCORI/Apal fragment of p3CGS-5 cDNA corresp. to p3CGS-5 nucleotide position numbers 1-452. Forty putative clones were picked from this first screen, of which six were randomly selected and purified. Each of the clones was spotted onto a lawn of host XLI cells and screened with a 370 bp PstI/Smal fragment of p3CGS-5 cDNA. Six putative clones were obtd. and sequenced. Clone pBBCGSPDE-7 contains an insert contg. an ORF encoding a 942 residue protein that is nearly identical to the adrenal gland cGS-PDE isozyme. The difference in the primary structure of these two isozymes lies in the amino terminal residues 1-46 of the brain cGS PDE and residues 1-25 of the adrenal cGS PDE. The remaining carboxy-terminal residues of the brain and adrenal cGS PDE are identical. (Updated on 25-
                                                                                                                                                                                                                                                                                    encoding mammalian cyclic nucleotide phospho-di:esterase - and vectors and host cells, useful for screening cpds. for inhibitory
                                                                                                                                                                                                                                                                                                                                                  Example 5B; Page 91; 133pp; English
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DQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT
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                                                 GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
                                                                 GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
                                                                                                           EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
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Cyclic GMP; stimulated; cyclic; nucleotide; bovine brain; phosphodiesterase; hybridisation; ss.

PDE from bovine brain clone pBBCGSPDE-7.

CGS

(revised)
(first entry)

25-MAR-2003 19-MAR-1993

AAR28408;

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AAQ83978 encodes AAR69729 the human cyclic-GMP stimulated nucleotide phospho-diesterase (CaM PDB) clone HFB9.2. Eukaryotic cells that express CaM PDE can be used to screen cpds. for the ability to modulate CaM PDE activity. CaM PDBs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers. Antibodies raised against CaM PDE can be used for enzyme purifcn., or determination. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the cyclic GMP stimulated phosphodiesterase (GGS -PDE) clone pHcgs6n isolated from human foetal brain. The cyclic nucleotide phosphodiesterases (PDEs) catalyse the hydrolysis of 3', 5' cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'- nucleotide monophosphates. The PDEs are therefore important in the control of the cellular concentration of cyclic nucleotides. The PDEs are, in turn, regulated by transmembrane signals or second messenger are, in turn, regulated by transmembrane signals or second messenger cole in regulating the flow of information from extracellular hormones, neurotransmitters, or other signals that use the cyclic nucleotides as messengers. PDEs are present in most of the cells and tissues of cherapeutic organisms, but only in trace amounts. cGS-PDEs are stimulated by cGMP in effecting cAMP hydrolysis. This is thought to occur through a concatalytic cGMP-specific site present on the cGS-PDE. The cDNA encoding this sequence can be used for the production of recombinant cGS-PDE, which may have therapeutic and diagnostic uses. This protein may also be useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP; adrenal gland; cGMP; transmembrane signal; extracellular hormone; neurotransmitter; antibody; human.
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                                                           941
                                                  900 HKFTIRGLPSNNSLDFLDEEYEVPDLDGTRAPINGCCSLDAE
                                    901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
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                                                                                                                                                                                                    pHcgs6n cyclic GMP stimulated phosphodiesterase.
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92US-00872644.
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Best Local Similarity 96.0
Matches 904; Conservative
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17-MAR-1997
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                      SGLQRAVKEALSAVLPRVETVYTYLLDGESQLVCEDPPHELPQEGKVREAIISQKRLGCN
                                                                                                           300 VEDKKSIQLKDLTSEDVQQLQSMLGCELQAMLCVPVISRATDQVVALACAFNKLEGDLFT
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                                                                                      GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
                                                                                                                                                                                                 DASSLOLKVLOYLQQETRASRCCLLLVSEDNLQLSCKV1GDKVLGEEVSFPL-TGCLGQV
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AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN
                                                                                                                                                                        EKHTLVALKRVQALQQRESSVAPEATQNPPEBAAGDQKGGVAYTDQDRKILQLCGELYDL
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ID AAW.
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AC AAW.
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DT 25-1
DT 05-2
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Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDB; assay; identification; modification; enzymatic activity; modulator; cyclic quanosine monophosphate-stimulated phosphodiesterase; cGS-PDB; human.
FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN
                                                                                                                                 600 FASFTYTPRSLPEDDISMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM
                                                                                                                                                                                                                                          FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM
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                                              FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN
                                                                                                                                                                 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY
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20-APR-1992;
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                                                                                                                                                                                                                                                                                                                                DNA encoding bovine and human phosphodiesterase enzymes - stimulated calcium/calmodulin, useful for recombinant prodn. of the enzymes.
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    ייייי שחשות יודשות phosphodiesterase; antibody; human; polymerase chain reaction.
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96.0%; Pred. No. 0;
ive 18; Mismatches 19; Indels
                                                                                                                                                                                                                                                         Beavo JA;
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                                                                                                                                                  94US-00297510.
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                                                               Homo sapiens
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The present sequence represents human cyclic guanosine monophosphatestimulated phosphodiesterase (CGS-PDE) CDNA. The specification also effectibes Ca2+/calmoduln sensitive cyclic nucleotide phosphodiesterase (Cam-PDE) enzymes. CaM-PDE enzymes catalyse the hydrolysis of cyclic nucleotides and as such control their intracellular level. They are controlled by second messengers e.g. Ca2+ and calmodulin and transmembrane signals and through pathways involving these, regulate flow of information from extracellular hormones, neurotransmitters and other signals using cyclic nucleotides as messengers. The specification describes an assay for identifying a chemical agent which modifies the enzymatic activity of a mammalian CaM-PDE. The assays are useful for identifying modulators of CaM-PDEs. The assays are useful for identifying explis expressing CaM-PDEs with the suspected modulator and messuring its effect e.g. monitoring the hydrolysis of cAMP and/or CGMP H flow 479 539 900 629 720 120 180 180 240 300 299 360 359 420 419 480 540 599 99 AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN 120 9 9 1 MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPQPCADSLQDALLSLGSVIDV SGLQRAVKBALSAVLPRVETVYTYLLDGESQLVCEDPPHELPQEGKVREAIISQKRLGCN GLGFSDLPGKPLARLVAPLAPDTQVLVMPLADKEAGAVAAVILVHCGQLSDNEEWSLQAV DASSLQLKVLQYLQQETRASRCCLLLVSEDNLQLSCKVIGDKVLGEEVSFPL-TGCLGQV VEDKKSIQLKDLTSEDVQQLQSMLGCELQAMLCVPVISRATDQVVALACAFNKLEGDLFT EARNLSNAEICSVFLLDQNELVAKVFDGGVVDDESYEIRIPADQIAGHVATTGQILNIP FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEBWSLQAV EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL DASSLQLKVLQYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLBEEISFPLTTGRLGQV VEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT DQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT EARNLSNAEI CSVFLLDONELVAKVFDGGVVEDESYEIRI PADOGIAGHVATTGOILNIP DAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN FASFTYTPRSLPEDDTSMAILSMLODMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM HAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDILLATDLAHHLRIFKD Gaps 1; DB 2; Length 941; Indels 19; Query Match 96.3%; Score 4728.5; Best Local Similarity 96.0%; Pred. No. 0; Matches 904; Conservative 18; Mismatches Sequence 941 AA; 181 61 61 121 121 181 241 241 300 361 360 421 420 481 480 541 540 601 909 661 099 721 301 88888888888888888 ò 윱 ઠે 엄 ઠે g ઠ 셤 g a 셤 ઠે 셤 ઠે g ઠે 셤 ò g ò 원 δ ઠ ઠે ð

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phosphodiesterase from the bovine brain. The phosphodiesterases isolated in this invention were used to transform host cells, preferably mammalian or yeast cells. The recombinant proteins and fragments produced can be used for therapeutic, diagnostic, and prognostic purposes and will provide the basis for preparation of monoclonal and polyclonal antibodies. An antibody specific for the Ca2+/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE) polypeptide is useful for affinity purification or detection of the polypeptide and is selective only for the Ca2+/calmodulin stimulated cyclic nucleotide PDE polypeptide 839 899 AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN 120 9 9 ò 840 MGNRPWEWDREKAYIPELQISFMEHIAMPIYKCLLQDLFPKAAELYERVASNREHWTKVS 780 LQKMAEVGYDRNNKQHHRLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFPSQGDLEKA MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS LQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPQPCADSLQDALLSLGSVIDV Gape purification cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n encodes 1, cow; Ca2+ stimulated phosphodiesterase;
Calmodulin stimulated phosphodiesterase; therapeutic; antibody. Length 941; 19; Indels 942 for Cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n. Bentley JK; HKFTIRGLPSNNSLDFLDEEYEVPDLDGTRAPINGCCSLDAE HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE - useful DB 2; Score 4728.5; Pred. No. 0; 8; Mismatches Antibody to phosphodiesterase polypeptide detection of polypeptide. Beavo JA, Example 6; Column 89/96; 68pp; English Ź 18; protein; 941 Sonnenburg WK, Charbonneau H, 91US-0068B356. 92US-00872644. 94US-00297494. 96.3**%**; 96.0**%**; 95US-00455526 Best Local Similarity 96.0% Matches 904; Conservative (UNIW) UNIV WASHINGTON WPI; 1998-446185/38. AAW77042 standard; N-PSDB; AAV48205 Sequence 941 AA; 14-DEC-1998 31-MAY-1995; 20-APR-1992; 29-AUG-1994; 19-APR-1991; US5789553-A. 04-AUG-1998 AAW77042; 781 841 900 -901 н Query Match 8b. RESULT 15 The ઠ 셤 ઠે 셤 ઠ 셤 ò 셤 ð

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Search completed: June 26, 2005, 12:17:23 Job time : 121.813 secs

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 6, Sequence 6, Sequence 6,

Sequence 4 Sequence 2 Sequence 7

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Sequence 23, Sequence 23,

ALIGNMENTS

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APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marball, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/872,644

FILING DATE: 19920420

CLASSIFICATION NUMBER: US/07/872,644

FILING DATE: 04-APR-1991

ATORNEY/AGENT INFORMATION:

NAME: No. 5389527and, Greta E.

REPRENCINCE/DOCKET NUMBER: 35.302

REPRENCINCE/DOCKET NUMBER: 35.302

REPRENCINCE/DOCKET NUMBER: 37.806

TELEROMENICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEROMETION OF SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 942 anino acids

TYPE: AMINO ACID

TYPE: AMINO ACID
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STREET: Street
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US-09-883-825-39
US-09-883-825-39
US-09-754-250-2
US-09-754-250-2
US-09-99-016-7922
US-08-951-648-6
US-09-174-437-6
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Patent No. 5389527
GENERAL INFORMATION:
   , MOLECULE TYPE: protein US-07-872-644-43
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STATE: Illinois
COUNTRY: USA
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     43, Appl
43, Appl
43, Appl
43, Appl
43, Appl
45, Appl
46, Appl
46, Appl
46, Appl
47, Appl
48,                                                                                                                            June 26, 2005, 12:10:37; Search time 30.8438 Seconds (without alignments) 2279.856 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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DB 1; Length 942;

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100.0%; Pred. No. 0; tive 0; Mismatches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:

LENGTH: 942 amino acids TYPE: amino acid

MOLECULE TYPE: protein

TOPOLOGY:

MEDIUM TYPE: FLOPMY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIS PC-DOS/MS-DOS
SOFTWARE: PATCHIS RC-BAS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTCRNEY/AGRNT INPORMATION:
NAME: NO. 5580771and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1190RMATION:
TELECOMMUNICATION 1305 #46-5750

STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago CITY: Chicago COUNTRY: USA

ZIP: 60603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS;
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray
ADDRESSEE: Bicknell

Joseph A.

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120
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DB 1; Length 942;
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 100.0%; Score 4911;
100.0%; Pred. No. 0;
                                0; Mismatches
              Best Local Similarity 100.
Matches 942; Conservative
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RESULT 2
US-08-297-494-43

Sequence 43, Application US/08297494

Patent No. 5580771

GENERAL INFORMATION:

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LQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA 840
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                           27866/30822
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302.
REFERENCE/DOCKET NUMBER: 27866,
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 984-9740
TELEFAX: (312) 984-9740
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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Matches 942; Conservative
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; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
APPLICANT: Charbonneau, Harry
APPLICANT: Charbonneau, Harry
; APPLICANT: Somenburg, William K.
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: Two First National Plaza, 20 South Clark STREET: Chicago
STATE: Illinois
COUNTY: USA
ZIP.
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ZIP: 60603
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
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US-08-297-510-43
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                                       GLGPSDLPGKPLARLVAPLAPDTQVLV1PLVDKEAGAVAAV1LVHCGQLSDNEEWSLQAV
                                                              GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
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APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Charbonneau, Harry
APPLICANT: Charbonneau, Harry
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEGUENCES: 58
ADDRESSES: Marshall, O'Toole, Gerstein, Murray
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                                                                                  941 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
                                                          MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                              Sequence 43, Application US/08479532
Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Carbonneau, Harry
APPLICANT: APPLICANTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Mur
APPLICANT: Two First National Plaza, 20 South
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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; Pred. No. 0;
0; Mismatches
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APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: 07/688,356
FILING DATE: 04-APP-1991
ATONEY/AGENT INFORMATION:
NAME: NO. 5776752and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/3C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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US-08-479-532-43
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FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDBYTKLLHDGIQPVAALDSN 600
                                                                                                                                                                                                           HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY 720
                                                                                                                                                                                                                                                                                                                                                                                                    SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOKMAEVGYDRTNKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
                                                                                                                                                                                                                                                                                                          HAFSVSHFCYLLYKNLELTNYLEDMEI FALFI SCMCHDLDHRGTNNSFQVASKSVLAALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAYAHPLFYRGVDDSTGFRTRNILCFPIRNENQEVIGVAELVNKINGPWFSKFDEDLATA
                                                                                                                                                                                                                                                                                                                                                                         SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDILLATDLAHHLRIFKD
  DAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA
                                                                                                                                                                                   PASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPPYHNWM
                                                                                         FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN
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STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley,
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalia
TITLE OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/688,356
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; Patent No. 5800987
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APPLICATION NUMBER: 08/297,494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-455-525-43
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494
FILING DATE: 04-APR-1991
ATPORNEY/AGENT INFORMATION:
NAMME: NO. 5789553and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TTELEPHONE: (312) 984-9740
                        Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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100.0%; Pred. No. 0;
ative 0; Mismatches
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Best Local Similarity 100.
Matches 942; Conservative
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                                                                                                                                     ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
    Bicknell
ADDRESSEE: Bickne
STREET: Two First
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
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                                         942
                                                            901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
                                         901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                     APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
CORRESPONDENCE SB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 4911;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/297,494
FILING DATE: 08/297,494
FILING DATE: 08/297,494
FILING DATE: 08/297,494
ATTORNEY/AGENT INFORMATION:
NAME: No. 6015677and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37.302
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  Sequence 43, Application US/09139491; Patent No. 6015677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY.

ZIP: 66603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNTER: IBM PC COMpatible
TOWNTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Beavo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DASSLOLKVLQYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQV 300
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                                                                                                                                                                                                             Length 942;
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                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                           Score 4911;
Pred. No. 0;
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-386
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acids
                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                               Matches 942; Conservative
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDLUM ITER: FLOPY TIEN.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: UDARA:
APPLICATION NUMBER: 09/123,783
FILING DATE: cUnknown>
APPLICATION NUMBER: 09/29,494
FILING DATE: cUnknown>
APPLICATION NUMBER: 09/297,494
FILING DATE: O4-DARE.1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6642040and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 984-9740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-883-825-43
                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acids
                                                     ZIP: 60603
COMPUTER READABLE FORM
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Best Local Similarity 100.
Matches 942; Conservative
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                                                                            EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
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                                                      EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
                                                                                                                          DASSLOLKVLOYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQV
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Street
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAR 942
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Bentley, Kelley
Charbonneau, Harry
Sonneburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/09883825
Patent No. 6642040
GENERAL INFORMATION:
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US-09-883-825-43
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AMINO ACID
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Matches 942; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                              MOLECULE TYPE: protein
                                                                    linear
                                 LENGTH: 94
TYPE: AMIN
TOPOLOGY:
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PCT-US92-03222-43
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03222
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PCT-US92-03222-43
Sequence 43. Application PC/TUS9203222
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bearley, Kelley,
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, ADDRESSEE: Bicknell STREET: Two First National Plaza, 20 Sou STREET: Chicago STREET: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REPERENNE/DOCKET NUMBER: 27866/30822
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (3
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                              241 DASSLQLKVLQYLQQETRASRCCLLLVSEDNLQLSCKVIGDKVLGEEVSFPL-TGCLGQV
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                                                                                                VEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT
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; Sequence 45, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
    APPLICANT: Benavo, Joseph A.
    APPLICANT: Bentley, Kelley
    APPLICANT: Charbonneau, Harry
    APPLICANT: Charbonneau, Harry
    APPLICANT: Sonnenburg, William K.
    APPLICANT: Sonnenburg, William K.
    APPLICANT: Sonnenburg, William K.
    APPLICANT: Sonnenburg, William K.
    APPLICANT: DINVENTION: Phosphodiesterases
    NUMBER OF SEQUENCES: 58
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COUNTRY: USA
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                                                                                                       Sequence 45, Application US/07872644

Sequence 45, Application US/07872644

Sequence 45, Application US/07872644

Sequence 45, Application US/07872644

SEGUENT: Beavo, Joseph A.

APPLICANT: Bentley, Keelley

APPLICANT: Bentley, Keelley

APPLICANT: Bentley, Milliam K.

ITILE OF INVENTION: DAD Encoding Mammalian

TITLE OF INVENTION: DATO Encoding Marker CORRESSEE: Bicknell O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell O'Toole, Gerstein, Murray & STREET: Street

CITY: Chicago

STREET: Two First National Plaza, 20 South Clark

STREET: Street

CONTRY: USA

CONTRY: USA

CONTRY: USA

COMPUTER: IDINOis

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/688,356

FILING DATE: USA-ARE-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. 5389527and, Greta E.

REGISTRATION NUMBER: 27866/30822

TELEPHONE: TELEPHONE: 33.) Aff-F-F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 941 amino acide TYPE: AMINO ACID
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MOLECULE TYPE: protein
US-07-872-644-45
                                                                                                                   US-07-872-644-45
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780 LQKWAEVGYDRNNKQHHRLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
                                                                                                                                                                                                                                                                                840 MGNRPWEMMDREKAYIPELQISFWEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
                                                                                                                              SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
                                                                                                                                                                                                                                                        841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
                              SSEGSVMERHHPAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
                                                                                                                                                                         LOKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
          HAPSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY
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STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45, Application US/08297510
| Patent No. 5602019
| GENERAL INFORMATION:
| APPLICANT: Beavo, Joseph A. APPLICANT: Bentley, Kelley
| APPLICANT: Charbonneau, Harry
| APPLICANT: Charbonneau, Harry
| APPLICANT: Sonnenburg, William K. TITLE OF INVENTION: DNA Encoding Mammalian TITLE OF INVENTION: Phosphodiesterases NUMBER OF SEQUENCES: 58
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.3%; Score 4728.5; Best Local Similarity 96.0%; Pred. No. 0; Matches 904; Conservative 18; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (312) 984-9740
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
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STATE: Illinois
COUNTRY: USA
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TELEX: 2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5580771and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
RELEFAX: (312) 346-5750
TELEFAX: (312) 346-5760
TELEFAX: (312) 346-5760
TELEFAX: (312) 346-5760
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TYPE: ADDIOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 4728.5;
96.0%; Pred. No. 0;
iive 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-297-494-45
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Best Local Simil
Matches 904; C
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE CONFUTER: IBM PC COMPATIBLE COFFWALEN SYSTEM: PC-DOS/MS-DOS SOFFWALE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,532 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/297,494 FILING DATE: APPLICATION NUMBER: US 07/688,356
                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
              APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
UNDER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5776722and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEFONE: (312) 946-5750
TELEFAX: (312) 944-9740
TELEFAX: (312) 944-9740
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
Charbonneau, Harry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 941 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                             ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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STATE: Illinois
COUNTRY: USA
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                                     1 MGQACGHSILCRSQQYPAARPAEPRGQQVFLKFDEPPPPPQPCADSLQDALLSLGSVIDI
                                                                                                                      GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
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                  MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPQPCADSLQDALLSLGSVIDV
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Sequence 45, Application US/08479532
Patent No. 5776752
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley

RESULT 13 US-08-479-532-45

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121 GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV 180
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96.0%; Pred. No. 0;
tive 18; Mismatches
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5789553and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1046-9740
TELECA: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-526-45
                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local Simil
Matches 904; C
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                                                    DAYAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA
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 FSIYCGISIAHSLLYKKVNBAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN
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Sequence 45, Application US/0845526

Patent No. 5789533

GENERAL INFORMATION:
APPLICANT: Bearley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Backell; O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Barchell, Chark
STREET: Street
CITY: Chicago
STREET: Street
CITY: Chicago
STREET: Street
CITY: Chicago
STREET: Street
CONPUTER READABLE FORM:
BEDING TYPE: Illinois
COMPUTER: Illinois
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/455,526
FILING DATE: 31-ANY-1995
CLASSIFTCATION NUMBER: US 08/297,494
FILING DATE: 29-AUG-1994
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US-08-455-526-45
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             LOKMAEVGYDRNNKQHHRLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEPFSQGDLEKA
                                                 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
LOKMAEVGYDRTNKQHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
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                                                                                                     HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE 942
                                                                                                                     HKFTIRGLPSNNSLDFLDEEYEVPDLDGTRAPINGCCSLDAE 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 13-MAY-1995
PLIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE: 08/297,494
FILING DATE: 08/297,494
FILING DATE: 08/297,494
ATLING DATE: 08/297,494
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                             Sequence 45, Application US/0845525;
Patent No. 5800987;
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley,
APPLICANT: Carroomeau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SUNENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.3%; Score 4/20.5; Best Local Similarity 96.0%; Pred. No. 0; Matches 904; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: No. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
REBERENCE/DOCKET NUMBER: 27866/30
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60603
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-455-525-45
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US-08-455-525-45
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241 DASSLQLKVLQYLQQETRASRCCLLLVSEDNLQLSCKVIGDKVLGEEVSFPL-TGCLGQV
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                                                                                                          GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
                                                                                                                                                                                                               EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
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June 26, 2005, 12:21:57; Search time 117.308 Seconds (without alignments) 3087.987 Million cell updates/sec
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11: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                          US-10-697-894-43
                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 43, Appl	Sequence 43, Appl	Sequence 45, Appl	Sequence 45, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 39, Appl	Sequence 5, Appli	Sequence 39, Appl	Sequence 4, Appli
SUMMARIES	US-09-883-825-43	US-10-697-894-43	US-09-883-825-45	US-10-697-894-45	US-10-686-390-5	/ US-10-686-282-5	US-10-686-349-5	US-09-883-825-39	US-10-094-989-5	US-10-697-894-39	US-10-094-989-4
DB	6	16	σ	16	16	17	17	σ	13	16	13
* Query Match Length DB	942	942	941	941	941	941	941	921	921	921	908
* Query Match	100.0	100.0	96.3	96.3	96.3	96.3	96.3	94.8	94.8	94.8	92.3
Score	4911	4911	4728.5	4728.5	4728.5	4728.5	4728.5	4657	4657	4657	4530.5
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Sequence 78, Appli Sequence 2, Appli Sequence 2928, Ap Sequence 2944, Ap Sequence 30, Appl Sequence 30, Appl	440004	7,00%	444 · 404	Sequence 6, Appli Sequence 2, Appli Sequence 13, Appli Sequence 3, Appli Sequence 3, Appli Sequence 23, Appli Sequence 23, Appli Sequence 5, Appli
1-236-417- 1-094-989- 1-108-260A- 1-104-047- 1-771-833- 1-86-949-	US-09-89 US-10-1 US-10-2 US-10-1 US-09-89 US-09-89	US-10-168-402- US-10-746-197- US-09-420-190-1 US-10-440-998- US-10-440-998-	US-10-618-252- US-10-440-998- US-10-440-999- US-09-321-801-4 US-09-321-801-1 US-09-321-801-1 US-10-618-252-	14 US-10-168-402-6 4 US-10-202-1007-2 17 US-10-887-276-2 9 US-09-891-216-13 16 US-10-746-197-3 15 US-10-427-222-3 14 US-10-115-515-23 17 US-10-094-1688-5 17 US-10-771-833-1
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ALIGNMENTS

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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/123,783
APPLICATION NUMBER: 09/297,494
                                                                                                                                                                                                                                                                                                                                 STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                         APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
US-09-883-825-43
; Sequence 43, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60603
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           Street
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Query Match
100.0%; Score 4911;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA Encoding Mamma Phosphodiesterases
                                                                                                                                                                                                                                                                                                                                                                     Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQ ID NO: 05-10-697-894-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     ; Sequence 43, Application US/10697894; Publication No. US20040126866A1 GENERAL INFORMATION: APPLICANT: Beavo, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 942 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 58
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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FILING DATE: «Unknown»

APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: NO. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
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                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 4911; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-883-825-43
                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ 1D NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acid
TYPE: amino acid
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Best Local 8
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                                                                                                                                                             841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
                                                                    781 LOKWAEVGYDRINKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
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COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-OCC-2003
FILING DATE: 30-OCC-2003
APPLICATION NUMBER: US/99/123,783
FILING DATE: 28-July-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: CURNOWN-
APPLICATION NUMBER: 08/297,494
FILING DATE: CURNOWN-
APPLICATION NUMBER: US/98
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
Bicknell
                                                                                                                                                                                                                                                    901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE 942
                                                                                                                                                                                                                                                                                901 HKFTIRGLPSNNSLDFLDEEYEVPDLDGARAPINGCCSLDAE
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NAME: NOLANG, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
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                                                          AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN
                                                                                             GLGPSDLPGKPLARLVAPLAPDTQVLVIPLVDKEAGAVAAVILVHCGQLSDNEEWSLQAV
             MGQACGHSILCRSQQYPAARPAEPRGQQVFLKRDEPPPPPQPCADSLQDALLSLGSVIDV
                                             AGLQQAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN
                                                                                                            EKHTLVALKRVQALQQRESSVAPEATQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL
                                                                                                                                                           DASSLQLKVLQYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQV
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MGQACGHSILCRSQQYPAARPAEPRGQQVFLKPDEPPPPPPPCADSLQDALLSLGSVIDV
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Sequence 45, Application US/09893825 Patent No. US20020151024A1 GENERAL INFORMATION:

RESULT 3 US-09-883-825-45 APPLICANT: Beavo, Joseph A. Bentley, Kelley

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                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPES Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/883,825

FILING DATE: 18-Jun-2001

CLASSIFICATION NUMBER: 09/123,783

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: 09/27,494

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: US 07/688,356

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: US 07/688,356

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: US 07/688,356

FILING DATE: <UNKNOWN>

ARTORNEY/AGENT INFORMATION:

NAME: NO. US20020151024Aland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30822

TELECOMMUNICATION:

MANDER: NO. NUMBER: 27866/30822
                                                                                                                                                  South Clark
                                                                                                               Murray
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                                                                                                               Gerstein,
                                     Mammalian
                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstei
Bicknell
STREET: Two First National Plaza, 20
Charbonneau, Harry
Sonnenburg, William K.
INVENTION: DNA Encoding Mammal
Phosphodiesterases
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96.0%; Pred. No. 0;
ive 18; Mismatches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
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                                                                        NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS
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Best Local Similarity 96.0%
Matches 904; Conservative
                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                     Street
                                                                                                                                                                                                                          COUNTRY: USA
                                      TITLE OF
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                                                                    FILING DATE: CURKNOWN APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
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96.0%; Pred. No. 0;
iive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  ID NO: 45:
A APPLICATION DATA:
APPLICATION NUMBER: US/09/123,7
BILING DATE: 28-U11y-1998
APPLICATION NUMBER: 08/297,494
                                                                                                                                                                                                                                                                                                                         LENGTH: 941 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
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INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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Matches 904; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-Oct-2003
CLASSIFICATION: <UNknown>
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Charbonneau, Harry
Sonnenburg, William K.
INVENTION: DNA Encoding Mammalian
Phosphodiesterases
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US-10-697-894-45
Sequence 45, Application US/10697894
Publication No. US20040126866A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Rentley, Kelley
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CORRESPONDENCE ADDRESS:
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STATE: Illinois
COUNTRY: USA
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APPLICANT: Pfizer Inc.
APPLICANT: Pfizer Limited
APPLICANT: Maw, Graham Nigel
APPLICANT: Maw, Graham Nigel
APPLICANT: Wayman, Crancology Enter
TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
FILE REFERENCE: PC10343D
CURRENT APPLICATION NUMBER: US/10/686,282
CURRENT FILING DATE: 2003-10-15
PRIOR FILING DATE: 2000-11-08
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                                  GLGFSDLPGKPLARLVAPLAPDTQVLVMPLADKEAGAVAAVILVHCGQLSDNEEWSLQAV
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Publication No. US20050020547A1
GENERAL INFORMATION:
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US-10-686-390-5
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Best Local Similarity
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Best Local Similarity 96.0°
Matches 904; Conservative
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PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-05
PRIOR PRIOR APPLICATION NUMBER: GB 001563.9
PRIOR FILING DATE: 2000-07-12
PRIOR PRILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-11
PRIOR PRILING DATE: 2000-07-11
PRIOR PRILING DATE: 2000-07-11
PRIOR PRILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
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96.0%; Pred. No. 0;
tive 18; Mismatches
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Best Local Similarity 96.0
Matches 904; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HC
US-10-686-282-5
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APPLICANT: Pfizer Limited
APPLICANT: Pfizer Limited
APPLICANT: Maw, Graham Nigel
APPLICANT: May, Graham Nigel
APPLICANT: Wayman, Christopher Peter
TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
FILE REFERENCE: PC10343C
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: US/10/686,349
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-18
PRIOR PRILING DATE: 2000-02-18
PRIOR PELING DATE: 2000-02-18
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 001553.9
PRIOR PELING DATE: 2000-07-05
PRIOR PELING DATE: 2000-07-05
PRIOR PELING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-11
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                                                                                                                                                                                                                                                                                                                     MGNR PMEMMDREKAYI PELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS
                                        HAFSVSHPCYLLYKNLELTNYLEDIEIFALFISCMCHDLDHRGTNNSFQVASKSVLAALY
                                                                                                                                      SSEGSVMERHHFAQAIAILNTHGCNIFDHFSRKDYQRMLDLMRDIILATDLAHHLRIFKD
                                                                                                                                                                                                                                                                                    LOKWAEVGYDRINKOHHSLLLCLLMTSCDLSDQTKGWKTTRKIAELIYKEFFSQGDLEKA
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96.0%; Pred. No. 0;
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                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPES FLORY;

MEDIUM TYPES FLORY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/883,825

FILING DATE: 18-Jun-2001

CLASSIFICATION NUMBER: 09/123,783

APPLICATION NUMBER: 09/123,783

FILING DATE: -Unknown-
APPLICATION NUMBER: 185 07/688,356

FILING DATE: -UNKNOWN-
APPLICATION NUMBER: 35,302

REFERENTENTION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30822

TELEPHONE: (312) 346-5750

TELEPHONE: CALLOR OF TRUE
                                               STREET: Two First National Plaza, 20 South Clark
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98.9%; Pred. No. 0;
:ive 3; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
              ADDRESSEE: Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 921 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Matches 898; Conservative
                                                                    Street
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                                                                                                                                                        VEDKKSIQLKDLTSEDVQQLQSMLGCELQAMLCVPVISRATDQVVALACAFNKLEGDLFT
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AGLQQAVKBALSAVLPKVETVYTYLLDGESRLVCEEPPHELPQEGKVREAVISRKRLGCN
                  SGLORAVKEALSAVLPRVETVYTYLLDGESOLVCEDPPHELPOEGKVREAIISOKRLGCN
                                                                                                                                                                                                         DASSLQLKVLQYLQQETQASRCCLLLVSEDNLQLSCKVIGDKVLEERISFPLTTGRLGQV
                                                                                                                                                                                                                                                                              VEDKKS1QLKDLTSEDMQQLQSMLGCEVQAMLCVPV1SRATDQVVALACAFNXLGGDLFT
                                                                                                                                                                                                                                                                                                                                                 DODEHVIOHCFHYTSTVLTSTLAFOKEOKLKCECOALLOVAKNLFTHLDDVSVLLOEIIT
                                                                                                                                                                                                                                                                                                                                                                                                                     EARNLSNAEI CSVFLLDQNELVAKVFDGGVVEDESYEIRI PADQGIAGHVATTGQILNI P
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Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
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Patent No. US20020151024A1
GENERAL INFORMATION:
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US-09-883-825-39
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US-10-697-894-39
; Sequence 39, Application US/10697894
; publication No. US20040126866A1
; GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Bentley, Kelley
; Charbonneau, Harry
Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
: TITLE OF INVENTION: DNA Encoding Mammalian
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Publication No. US2020115179A1

GENERAL INCRNATION:

APPLICANT WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/094,989

CURRENT FILING DATE: 2002-03-12

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SERVING APPLICATION OF APPLI
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HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYFPRSLPEDDTSMAILSMLQDMNFINNYK 613
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Publication No. US2020115179A1;
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE;
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN;
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF;
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF;
TITLE OF INVENTION: DATE: 2001-031-12
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR APPLICATION NUMBER: 2001-01-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASESEQ for Windows Version 4.0
LODLPPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDBBYEVPDLDGARAPIN
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                                                                          HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK
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                                                                                                                                                                                                                                                674 MCHDLDHRGINNSFQVASKSVLAALYSSEGSVWERHHFAQAIAILNTHGCNIFDHFSRKD
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                                                                                                                                                  IDCPTLARFCLMVKKGYRDPPYHNWMAAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC
                                                                                                                                                                                                                                                                                                       YORMLDLMRDIILATDLAHHLRIFKDLOKMAEVGYDRTNKOHHSLLLCLLMTSCDLSDQT
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95.8%; Pred. No. 0;
iive 18; Mismatches
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Best Local Similarity 95.8%
Matches 868; Conservative
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TYPE: PRT
ORGANISM: Homo sapien
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US-10-094-989-4
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                                                                                                                                                      Version #1.25
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                     COMPUTER: ISAN GLASS ALSO
COMPUTER: ISAN COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PASTENTIN Release #1.0, Veri
SOFTWARE: PASTENTIN Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-OCT-2003
CLASSIFICATION NUMBER: US/09/123,783
APPLICATION NUMBER: US/09/123,783
FILING DATE: <UNFORMATION
APPLICATION NUMBER: US/09/1297,494
FILING DATE: <UNFORMATION
APPLICATION NUMBER: US/0587,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
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al Similarity 98.9%; Pred. No. 0;
898; Conservative 3; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                      ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 921 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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QKGGAAYTDRDRKILQLCGELYDLDASSLQLKVLQYLQQETRASRCCLLLVSEDNLQLSC
                   KVIGDKVLEEEISPPLTTGRLGQVVEDKKSIQLKDLTSEDMQQLQSMLGCEVQAMLCVPV
                              KVIGDKVLGEEVSFPL-TGCLGQVVEDKKSIQLKDLTSEDVQQLQSMLGCELQAMLCVPV
                                                          ISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEQKLKCECQA
                                                                       BIRIPADQGIAGHVATTGQILNIPDAXAHPLFYRGVDDSTGFRTRNILCFPIKNENQEVI
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Publication No. US20040048256A1
GENERAL INFORMATION:
APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBENCE: 21402-442C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT APPLICATION NUMBER: US60/318,120
PRIOR PILING DATE: 2001-09-01
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR PLICATION NUMBER: US60/318,180
PRIOR PLICATION NUMBER: US60/318,184
PRIOR PLICATION NUMBER: US60/318,184
PRIOR PLICATION NUMBER: US60/318,184
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR PLICATION NUMBER: US60/316,1663
PRIOR PLICATION NUMBER: US60/316,1663
PRIOR PLICATION NUMBER: US60/396,412
PRIOR PLICATION NUMBER: US60/396,412
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PRIOR APPLICATION NUMBER: US60/322,636
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/322,817
PRIOR APPLICATION NUMBER: US60/322,816
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
Remaining Prior Application data removed - 8; NUMBER OF SEQ ID NOS: 341
SEQ ID NO 78
LENGTH: 920
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                          KVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKID
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GVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2928, Application US/10108260A
; Sequence 2928, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; APPLICANT: HILAGORIE: MARRIT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2928
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92.9%; Pred. No. 0;
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Matches 827; Conservative
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US-10-108-260A-2928
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                                                                                                                                                                                                 Sequence 2, Application US/10094989;
Publication No. US2002011517941
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROPEDING, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROPEDINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROPEDINS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROPEDING, NUMBER: US/10/094,989
CURRENT APPLICATION NUMBER: US/10/094,989
CURRENT APPLICATION NUMBER: 09/754,250
FRIOR APPLICATION NUMBER: 09/754,250
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PREESE for Windows Version 4.0
SEQ ID NO 2
LENGTH: 920
              795 WKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQ
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WKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKULQ
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Best Local Similarity 94.99
Matches 860; Conservative
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ORGANISM: Homo sapien
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TITLE OF INVENTION: No. US20030236392Alel full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: WHICH CANDER SOFTHER STATES NUMBER: NUMBER OF SEQ ID NOS: 4096
SOFTHARE: Patentin Ver. 2.1
LENGTH: 786
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94.1%; Pred. No. 7e-274;
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Best Local Similarity 94.1%
Matches 672; Conservative
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Search completed: June 26, 2005, 12:41:01 Job time : 120.308 secs